## STIC-Biotech/ChemLib

From:

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Chan, Christina

Sent: To:

Tuesday, October 09, 2001 12:52 PM Davis, Minh-Tam; STIC-Biotech/ChemLib

Subject:

RE: Rush search request for 09/580523

## Please rush. Thanks Chris

From:

----Original Message-----Davis, Minh-Tam

Sent:

Tuesday, October 09, 2001 12:37 PM

T:

Chan, Christina

Subject:

Rush search request for 09/580523

Please search in commercial data base and issued patent file:

1) SEQ ID NO:1

2) SEQ ID NO:1, without Serine, or glycine or alanine at amino acid position 118.

3) SEQ ID NO:1 having alanine at amino acid position 118.

4) Amino acid sequence 103-123 of SEQ ID NO:1.

5) An amino acid sequence comprising the amino acid sequence 143-168 of SEQ ID NO:1, but no serine at amino acid position 118.

6) Please search SEQ ID NO:1 against the parent case 60/136783 for priority date.

Thank you MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Point of Contact: Jan Delevel Librarian-Physical Sciences

CM1 1E01 Tel: 308-4498

(CTGEU) **XNAJA 30A9 SIHT** 

Access	DB#	

## SEARCH REQUEST FORM

## Scientific and Technical Information Center

Requester's Full Name	:	Examiner = :	Date:
Art Unit:	Phone Number 30	Serial Number:	
Mail Box and Bldg/Ro	om Location:	Serial Number: Results Format Preferred (circle):	PAPER DISK E-MAIL
f more than one sea	rch is submitted, please	prioritize searches in order of ne	ed.
nclude the elected species utility of the invention. De	or structures, keywords, synony	describe as specifically as possible the sub ims, acronyms, and registry numbers, and e special meaning. Give examples or relevan laims, and abstract.	ombine with the concept or
Title of Invention:			
	e full names):		
		1	
Earliest Priority Filing	Date:		
*For Sequence Searches Or appropriate serial number.	ily* Please include all pertinent in	formation (parent, child, divisional, or issued p	atent numbers) along with the

Point of Contact:
Jan Delaval
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

STAFF USE ONLY	Type of Search	Vendors and cost where applicable	
Searcher	NA Sequence (#)	STN	
Searcher Phone = ung 8	AA Sequence (#)	Dialog	
Searcher Location.	Structure (#)	Questel:Orbit	
Date Searcher Picked Up 10 19	Bibliographic	Or Link	
Date Completed 10 9	Litigation	Lexis/Nexis	
Searcher Prep & Review Time	Fulltext	Sequence Systems	
Clencal Prep Time	Patent Family	WWW/Internet	
Online Time. 30	Other	Other (specify)	

PTO-1590 (1-2000)

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Appli

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Sequence 5, Appli
Sequence 5, Appli
Patent No. 5516630
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Acids and Methods of Use
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STAFE: California
COUNTRY: United States
LIP: 22121
                        Sednence Sed
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 145; DB 2; Best Local Similarity 100.0%; Pred. No. 3.6e-14; Matches 26; Conservative 0; Mismatches 0;
                        US-09-007-383-16

US-08-325-847-4

US-08-188-587-32

US-08-646-715-32

US-08-76-741B-79

US-08-72-24-179

US-08-924-695-79

US-08-614-935-29

US-08-614-935-29

US-08-614-156B-1

US-08-087-016-4

US-08-087-016-4

US-08-087-016-5

US-08-087-016-5

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US-08-087-016-5

US-08-087-016-5

US-08-087-016-5

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US-08-087-016-5

US-08-08-097-016-6

US-08-08-097-016-6

US-08-08-097-018-6
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CLASSIFICATION: 435

ATTONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 QSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08717123 Patent No. 5965703
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amino acid
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28, Appl
20, Appl
110, App
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20.598 Million cell updates/sec
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Sequence 14,
Sequence 3,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-717-123-2
US-08-985-335-1
US-08-985-335-7
US-08-333-565-2
US-08-333-565-2
US-08-733-505A-12
US-08-733-505A-14
US-08-733-505A-14
US-08-733-505A-14
US-08-733-505A-14
US-08-733-505A-14
US-08-661-479-28
US-08-661-479-28
US-08-614-935-28
US-08-614-935-28
US-08-614-935-28
US-08-133-288-20
US-08-133-288-20
US-08-133-287-28
US-08-133-288-20
US-08-133-288-20
US-08-133-288-20
US-08-029-333-15
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                                                                                                                                                                                                                                                                                                                                                                                     26
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                                                                                                                                                                                                                                                                                                                                                                                  1 QSSSWTRVFQSWWDRNLGRGSSAPSQ
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                       October 9, 2001, 15:52:36
                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2

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Gaps

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US-08-665-617-2

Sequence 2, Application US/08665617

Sequence 1, Patent No. 566316

SERENAL INFORMATION:

APPLICANT: Xudong, Yin

TITLE OF INVENTION:

Gene and Protein for Regulation of Cell Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                . rurk:

. cumputer: Diskette

. cumputer: IBM Compatible

) OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,335

FILING DATE: Filed Herewith

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/APTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 145; DB 3;
nilarity 100.0%; Pred. No. 3.6e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik STREFI: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                      3: Incyte Pharmaceuticals, Inc.
3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/665,617
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NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: 12LEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166 INFORMATION FOR SEQ ID NO:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 26; Conserv
                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INELLIBRARY: General 1683637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Gainesvil
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL TITLE OF INVENTION: PROLIFERATION NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 145; DB 3;
Pred. No. 3.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASISED FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE:
ATTORNEY, AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0421 US
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                        E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 QSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                          Sequence 1, Application US/08985335
Patent No. 6080847
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US-08-985-335-7
; Sequence 7. Application US/08985335
; Patent No. 6080847
                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 26; Conservative 0;
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INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yue, Henry
APPLICANT: Al, Preeti
APPLICANT: Shah, Purvi
APPLICANT: COTIEY, Neil C.
TITLE OF INVENTION: PROLIFEI
NUMBER OF SEQUENCES: 9
                                                                                                                                             APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: SYNORAB01
CLONE: 358673
                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                        US-08-985-335-1
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GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEX J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                 Sequence 2, Application US/08661479
Fatent No. 5834209
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: REGULATOR
TITLE OF INVENTION: REGULATOR
ORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 7379 Lytton Avenue
CITY: Palo Allo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Deduced amino acid sequence of mouse BAD."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-3UN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATE: US/08/661,479
FILING DATE: 31-0CT-1994
ATTON NUMBER: 31-0CT-1994
ATTON NUMBER: 31-0CT-1994
ATTON NUMBER: 30.223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFACE (415) 326-2400
TELEFACE (415) 326-2422
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.8%; Score 120; DB 2; 73.1%; Pred. No. 2.1e-10; ive 3; Mismatches 4
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
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Best Local Similarity 73.1
Matches 19; Conservative
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-661-479-2
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STRANDEDNESS: sin
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                                                                                                                      RESULT 6
US-08-661-479-2
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Pred. No. 2.1e-10;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                            95.9%; Score 139; DB 1; Length 166; 92.3%; Pred. No. 2.7e-13;
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                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl.x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-OCT-1994
ATTONNEY/AGENT INFORMATION:
NAME: SMITH WIlliam M
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET UNMER: 15726A-000700
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION OF SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
REFERENCE/DOCKET NUMBER: CL-8
            TELECOMMUNICATION INFORMATION:
TELEPHONE: (152) 375-8100
TELEFAX: (152) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08333565
Patent No. 5622852
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73.18;
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Best Local Similarity 73.1
Matches 19; Conservative
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linear
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MOLECULE TYPE: protein
US-08-665-617-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION:
US-08-333-565-2
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Matches 24; Conserva
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US-08-333-565-2
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Patent No. 5856445
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERRAMP, L.C.
STREET: 7733 PORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOCOMMON
                         TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 73.1
Matches 19; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                     linear
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Best Local Similarity
Matches 19; Conserv
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TOPOLOGY: li
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   TELEPHONE:
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Patent No. 5856445
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.8%; Score 120; DB 2;
73.1%; Pred. No. 2.1e-10;
iive 3; Mismatches 4;
                                                      ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLNU DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRPE: amino acid
STRPE: amino acids
STRPE: amino acids
STRPE: amino acids
STRPE: ACCOUNTY ACCOUNT
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                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFRENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.8'
Best Local Similarity 73.1'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
NUMBER OF SEQUENCES:
                                                                                  STREET: 7733 FOR:
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                        ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63105
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US-08-733-505A-12
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Pred. No. 2.1e-06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCJ-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 120; DB 2; 73.1%; Pred. No. 2.1e-10; ive 3; Mismatches 4;
US/08/717,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 QSAGWTRIIQSWWDRNLGKGGSTPSQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08333565 Patent No. 5622852
           FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID
TELECOMMUNICATION INPORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION UNUBER: 30,23
REFERENCE/DOCKET UNUBER: 15726
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 326-2400
TELEFRAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.9%;
80.0%;
                                                                                                                                                                                                                                                          1: 204 amino acids amino acid
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Best Local Similarity 73.1
Matches 19; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-333-565-17
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-717-123-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-08-333-565-17
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                                                                     THILE OF INVENTION: STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL. XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 PCRSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
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Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic TITLE OF INVENTION: Acids and Methods of Use NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 2;
Pred. No. 2.1e-10;
3; Mismatches 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
           Sequence 14, Application US/08733505A Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314) 727-5188
TELEFRX: (314) 727-6092
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 204 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 73.18
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Sequence 28, Application US/O8661479

Patent No. 5834209

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION NUMBER: US/08/661,479
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/33,565
FILING DATE: 31-OCT-1994
ATTONINEY/AGENT INPOMBER: US
NAME: SMITH, William M
REGISTRATION NUMBER: 30,223
                                   COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
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APPLICATION. 435
FILING DATE: 31-C.
FILING DATE: 31-C.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15726A-000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.9%; Score 81; 75.0%; Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 12; Conserv
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US-08-333-565-28
Sequence 28, Application US/08333565
Fatent No. 5622852
GENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                 Sequence 17, Application US/08661479
Patent No. 5814209
GENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
21P: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/33,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUTCATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2420
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84; DB 2; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 amino acids
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-661-479-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 WTRIIQSWWDRNLGK 16
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2 WTRIIQSWWDRNLGK 16
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5 WTRVFOSWWDRNLGR 19
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STREET: 3/2 L.
CITY: Palo Alto
TATE: California
                                                                                                                              US-08-661-479-17
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SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: peptide
US-08-661-479-28
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0; Gaps Query Match 55.9%; Score 81; DB 2; Length 16; Best Local Similarity 75.0%; Pred. No. 5.9e-06; Matches 12; Conservative 2; Mismatches 2; Indels

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2 SSSWTRVFQSWWDRNL 17 |:|||:|||||||||||| 1 SAGWTRIIQSWWDRNL 16 ŏ

q

Search completed: October 9, 2001, 15:52:36 Job time: 151 sec

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6, Appli 15614, A 31748, A 16, Appl 836, App 11888, A 12815, A 5757, Ap 6570, Ap 9756, Ap 13250, A

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Sequence 1777, Ap
Sequence 1965, Ap
Sequence 579, App
Sequence 408, App
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Sequence 2, Application US/09922378

Sequence 2, Application US/09922378

GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES,
CURRENT APPLICATION NUMBER: US/09/922,378

CURRENT APPLICATION NUMBER: US/09/922,378

CURRENT FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09922378

GENERAL INFORMATION:

APPLICANT: Horne, William A.

APPLICANT: Oltersdorf, Tilman

TITLE OF INVENTION: ACIDS AND POLYPEPTIDES, ENCODING NUCLEIC

TITLE OF INVENTION: ACIDS AND METHODS OF USE

FILE REFERENCE: 480140.42803

CURRENT APPLICATION NUMBER: US/09/922,378

CURRENT FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 3

LENGTH: 204
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             US-09-895-814-895-
US-09-895-814-932
US-09-806-428-6
US-09-902-540-15614
US-09-945-258-16
US-09-945-258-16
US-09-760-446-1965
US-09-760-446-1965
US-09-760-446-1965
US-09-758-470-408
US-09-758-470-408
US-09-768-470-408
US-09-768-470-408-1188
US-09-768-470-408-1188
US-09-764-470-4708-1188
US-09-764-470-4708-1188
US-09-764-470-4708-1188
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Pred. No. 3.7e-12;
Mismatches 0;
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US-09-803-110-13250
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CORGANISM: Homo sapiens
US-09-922-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
US-09-922-378-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 26; Conserv
LENGTH: 168
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Sequence 58580, A
Sequence 37015, Ap
Sequence 114, App
Sequence 10865, App
Sequence 9450, Ap
Sequence 7468, Ap
Sequence 12532, A
Sequence 12532, A
Sequence 1103, Ap
Sequence 1103, Ap
Sequence 1103, Ap
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Sequence 3, Appli
Sequence 2762, Ap
Sequence 56706, A
                                                                                                                                                 (without alignments)
33.961 Million cell updates/sec
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Sequence 897, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                             ; Search time 36.31 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/3/paa_NPCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/3/paa_NUS06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/3/paa_NUS08_NEW_COMB.pep:*

3: /cgn2_6/ptodata/3/paa_NUS08_NEW_COMB.pep:*

3: /cgn2_6/ptodata/3/paa_NUS08_NEW_COMB.pep:*

3: /cgn2_6/ptodata/3/paa_NUS08_NEW_COMB.pep:*

3: /cgn2_6/ptodata/3/paa_NUS09_NEW_COMB.pep:*
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Compugen Ltd
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PCT-USO1-08631-56706
US-09-9617-681A-7103
PCT-USO1-08631-56706
US-09-617-681A-7103
PCT-USO1-08631-58580
US-09-617-681A-7103
PCT-USO1-08631-58580
US-09-788-356-114
US-09-788-356-114
US-09-788-356-114
US-09-788-356-1103
US-09-6865-768
US-09-6868-1103
US-09-6868-1103
US-09-69-866A-1103
US-09-895-793-897
US-09-895-793-897
US-09-895-793-897
US-09-895-793-894
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       311045 seqs, 47428042 residues
                                                                                                                                                                                                                         145
1 QSSSWTRVFQSWWDRNLGRGSSAPSQ
               GenCore version Copyright (c) 1993 - 2000
                                                                                                                                                                                                      US-09-580-523-1_COPY_143_168
                                                                                                                           October 9, 2001, 16:08:31
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match I
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No.
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Gaps

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RESULT 5
US-09-617-681A-7103
Sequence 7103, Application US/09617681A
Sequence 7103, Application US/09617681A
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Thereby
FILE REPRENCE: 2750-1064P
CURRENT APPLICATION NUMBER: US/09/617,681A
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 9311
SEQ ID NO 7103
LENGTH: 10?
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WHER INFORMATION: Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins domain OTHER INFORMATION: identified by eMATRIX, accession number BL01009C, p-value=1.78 OTHER INFORMATION: 12, raw score of 10.54
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILLE REPERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 58580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 103;
                                                                   Length 66;
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                                                                   DB 1;
3.7;
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                                                               Query Match 35.9%; Score 52; DB Best Local Similarity 50.0%; Pred. No. 3.7, Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..103
CTHER INFORMATION: Ceres Seq. ID 1437722
NAME/KEY: misc_feature
LOCATION: 1..103
CHER INFORMATION: Xaa is any amino acid
US-09-617-681A-7103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
PCT-10501-08631-58580
PCT-10501-08631-58580, Application PC/TUS0108631
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SSWTRVFQSWWDRNL-----GRG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 SAWV----AWWDRNLCGIHGGGRG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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LOCATION: (20)..(75)
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PCT-US01-08631-56706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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LOCATION: (146)
NAME/KEY: SITE
LOCATION: (169)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids PCT-0501-18569-2762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55706, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                 APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PAIJ3PCT
CURRENT APPLICATION NUMBER: PCT/USO1/18569
CURRENT FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 2.0
                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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OTHER INFORMATION: Xaa = X or * as defined in Table 2
Best Local Similarity 73.1%; Pred. No. 9.4e-09; Matches 19; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                             RESULT 3
PCT-USO1-18569-2762
PCT-USO1-18569-2762, Application PC/TUS0118569
GENERAL INFORMATION:
                                                                                        1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QSSSWTRVFQSWWDRNLGRGS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)...(66)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US01-08631-56706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 56706
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2762
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                                       3 SSWTRVFQSWWDRNL----GRGSSAPS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/09784356
GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1030 QSSSRFYVVMWKQVTQSYWDIN 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QSSS-----WTRVFQSWWDRN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.5%;
Best Local Similarity 50.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-09-784-356-114
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US-09-758-447-658
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OTHER INFORMATION: SCP-like extracellular protein domain identified by PFan
OTHER INFORMATION: accession name SCP, E-value=1.1e-18, PFam score of 71.1
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (14); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-446-1130
                                                                                                                                                                                                            Gaps
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PMO19
CURRENT APPLICATION NUMBER: US/09/758,446
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 1734
SOFTWARE: PALENTIN VON: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37015, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 140;
                                                                                                                                                                   Length 97;
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                                                            COCATION: (1)...(97)
COTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-58580
                                                                                                                                                                   DB 1;
9.8;
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14;
                                                                                                                                                                 Score 50; DB Pred. No. 9.8; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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illarity 40.9%; Pred. No.
Conservative 4; Mismatc
                                                                                                                                                                                                                                                 3 SSWTRVFQSWWDRNL----GRGSSAPS 25
                                                                                                                                                                                                                                                                                                                                                                       US-09-758-446-1130; Sequence 1130, Application US/09758446; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          48 TSWSSAIQSWYDEILDFVYGVGPKSPN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 TWWPISRSWWTRAPCRWASPPS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SWTRVFQSWWDRNLGRGSSAPS 25
                                                                                                                                                                 Query Match 34.5%;
Best Local Similarity 37.0%;
Matches 10; Conservative
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Best Local Similarity
'-has 9; Conserv?
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LENGTH: 257
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LOCATION: (149)...(170)
CTHER INFORMATION: Extracellular proteins SCP/Tpx-1/Aq5/PR-1/Sc7 proteins domain
CTHER INFORMATION: 1dentified by eMATRIX, accession number BL01009D, p-value=9.47
OTHER INFORMATION: 23, raw score of 14.19
NAME/REY: DOMAIN
LOCATION: (17)...(191)
OTHER INFORMATION: SCP-like extracellular protein domain identified by PFam,
CTHER INFORMATION: accession name SCP, E-value=7.9e-97, PFam score of 335.1
PCT-US01-08631-37015
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APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Wotson, Susan R.
APPLICANT: BOS Biotechnology, Inc.
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
TITLE OF INVENTION: Modulators
CURRENT APPLICATION NUMBER: US/09/784,356
CURRENT APPLICATION NUMBER: US 60/148,425
PRIOR APPLICATION NUMBER: US 60/148,425
PRIOR APPLICATION NUMBER: US 09-08-11
PRIOR APPLICATION NUMBER: US 09-08-11
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PM028
; CURRENT APPLICATION NUMBER: US/09/758,447
; CURRENT FILING DATE: 2001-01-11
; PRIOR PAPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR PLILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 812
; SCFTWARE: Patentin Ver. 2.0
; SEQ ID NO 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 5; Length 1170;
Pred. No. 99;
2; Mismatches 3; Indels
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R APPLICATION NUMBER: 60/249, 299
R FILING DATE: 2000-11-17
R PILING DATE: 2000-11-17
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241, 785
R APPLICATION NUMBER: 60/241, 785
R APPLICATION NUMBER: 60/24, 617
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/25, 268
R APPLICATION NUMBER: 60/25, 268
R APPLICATION NUMBER: 60/25, 348
R FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/25, 344
R FILING DATE: 2000-10-08
R APPLICATION NUMBER: 60/229, 344
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229, 345
R APPLICATION NUMBER: 60/229, 369
R APPLICATION NUMBER: 60/231, 413
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R APPLICATION NUMBER: 60/237,040
R APPLICATION NUMBER: 60/240,960
R FILING DATE: 2000-10-20
R FILING DATE: 2000-10-20
R FILING DATE: 2000-10-13
R FILING DATE: 2000-10-13
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APPLICATION NUMBER: 60/241,787
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,474
FILING DATE: 2000-11-08
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FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
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APPLICATION UNMBER: 60/226,681
FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/225,759
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                                                                       2000-10-20
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                      FILING DATE: 2000-0'
APPLICATION NUMBER:
FILING DATE: 2000-10
PRIOR
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                                                               NAME/KEY: SITE
LOCATION: (461)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-447-658
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APPLICANT: NOGENION:

TITLE OF INVENTION:

FILE REPERENCE:

FOR CURRENT PRICATION NUCLEIC ACIDS, Proteins, and Antibodies

FULE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/764,905

PRIOR PELION DATE: 2001-01-17

PRIOR PELION DATE: 2000-02-04

PRIOR PELION DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR PELION DATE: 2000-05-28

PRIOR PELING DATE: 2000-06-28

PRIOR PELING DATE: 2000-06-28

PRIOR PELING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR PELING DATE: 2000-07-26

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR PELING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,447

PRIOR PELING DATE: 2000-07-14

PRIOR PELING DATE: 2000-07-16

PRIOR PELING DATE: 2000-07-17

PRIOR PELING DATE: 2000-07-17

PRIOR PELING DATE: 2000-07-14

PRIOR PELING DATE: 2000-07-14
                                                                                                                                                                                                                   Length 1223;
                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                   Score 50; DB 5;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                 2; Mismatches
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PRIOR FILING DATE: 2000-07-07
PRIOR PELLING DATE: 2000-08-10
PRIOR PILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/25,869
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,84
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Sequence 10865, Application US/09764905
GENERAL INFORMATION:
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RRIOR FILING DATE: 2000-09-29
FRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
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PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/234,223
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                                                                                                                                                                                                                                                                                                                 1 QSSS-----WIRVFQSWWDRN 16
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Best Local Similarity 50.0%;
Matches 11; Conservative
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                      ORGANISM: Homo sapiens
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                                             FEATURE:
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DR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/232,401

DR FILING DATE: 2000-09-14

DR PELLORD DATE: 2000-09-14

DR PELLORD DATE: 2000-10-20

DR APPLICATION NUMBER: 60/241,808

DR APPLICATION NUMBER: 60/241,808

DR APPLICATION NUMBER: 60/241,786

DR APPLICATION NUMBER: 60/241,786

DR APPLICATION NUMBER: 60/241,221

DR APPLICATION NUMBER: 60/241,231

DR APPLICATION NUMBER: 60/241,231

DR APPLICATION NUMBER: 60/241,231
                                          NR FILING DATE: 2000-09-27

NR APPLICATION NUMBER: 60/230,438

NR APPLICATION NUMBER: 60/215,135

NR APPLICATION NUMBER: 60/215,135

NR FILING DATE: 2000-06-30

NR APPLICATION NUMBER: 60/225,266

NR APPLICATION NUMBER: 60/225,266

NR APPLICATION NUMBER: 60/249,218

NR APPLICATION NUMBER: 60/249,218
                                                                                                                                                                                                                                                                                             FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,245
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,244
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/233,064
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/233,063
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/225,214
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/235,836
                                                                                                                                                                                     APPLICATION NUMBER: 60/249, 208 FILING DATE: 2000-11-17
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LING DATE: 2000-11:17
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APPLICATION WUMBER: 60/249,212
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,207
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ILING DATE: 2000-11-17
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PLICATION NUMBER: 60/231,242
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PPLICATION NUMBER: 60/232,081
ILING DATE: 2000-09-08
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PPLICATION NUMBER: 60/232,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/233,065
FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                        PPLICATION NUMBER: 60/249,211
ILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILING DATE: 2000-11-17
.PPLICATION NUMBER: 60/249,264
ILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICATION NUMBER: 60/249,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLICATION NUMBER: 60/249,297
LING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICATION NUMBER: 60/231,414
ILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICATION NUMBER: 60/231,244 ILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/232,397
                                                                                                                                                                                                                                                                                                                                                                                           LING DATE: 2000-11-1
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LOCATION: (75)...(93)
OTHER INFORMATION: Extracellular proteins SCP/Tpx-1/Aq5/PR-1/Sc7 proteins domain OTHER INFORMATION: identified by eMATRIX, accession number BL01009A, p-value=9.57 OTHER INFORMATION: 16, raw score of 13.75
NAME/KEY: DOMAIN
LOCATION: (17)...(154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (17)...(154)
OTHER INFORMATION: SCP-like extracellular protein domain identified by PFam,
OTHER INFORMATION: accession name SCP, E-value-1.1e-60, PFam score of 215.1
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OTHER INFORMATION: Bukaryotic RNA-binding region RNP-1 proteins domain
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ;
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                                                   Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                              Sequence 37014, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR ELLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR PPLICATION NUMBER: 09/577,408
PRIOR PILING DATE: 2000-05-18
NUMBER OF SEQ. ID NOS: 16102
SOFTWARE: Custom
                                                Query Match 33.8%; Score 49; DB 5; Best Local Similarity 50.0%; Pred. No. 5.4; Matches 7; Conservative 2; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.8%; Score 49; DB Best Local Similarity 38.5%; Pred. No. 22; Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9450, Application PC/TUS0114827 GENERAL INFORMATION:
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; PRIOR APPLICATION NUMBER: 60/232,398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
                                                                                                                                               10 QSWWDRNLGRGSSA 23
                                                                                                                                                                              11 QGWWESRVGRGREA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                               PCT-US01-08631-37014
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LENGTH: 168
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Gaps

7;

Length 209; 7; Indels

DB 1;

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// NAME/KEY: misc_feature
// LOGATION: (1)...(209)
// OTHER INFORMATION: Xaa = X or * as defined in Table
PCT-US01-08656-7468
                                                                                                                                                                                                                                                                                       33.4%; Score 48.5; C
40.6%; Pred. No. 32;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          2 SSSWTRVFQS-----WWDRNLGR-GSSAPSQ 26
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Job time: 382 sec
                                                                                                                                                                                                                                                                                       Query Match 33.4
Best Local Similarity 40.6
Matches 13; Conservative
                                                            TYPE: PRT
ORGANISM: Homo sapiens
             SEQ ID NO 7468
                                    LENGTH: 209
                                                                                                             FEATURE:
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OTHER INFORMATION: identified by eMATRIX, accession number BL00030B, p-value=9.526e-
OTHER INFORMATION: 09, raw score of 7.03
NAME/RET: DOWAIN
OTHER INFORMATION: RNA recognition motif. domain identified by PFam, accession
OTHER INFORMATION: name rrm, E-value=6.1e-15, PFam score of 63.1
NAME/RET: insc_feature
NAME/RET: insc_feature
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (649)...(669)
CTHER INFORMATION: CORONAVIRUS NUCLEOCAPSID PROTEIN domain identified by OTHER INFORMATION: eMATRIX, accession number DM01206B, p-value=4.646e-09, raw score PCT-US01-08656-8991
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GENERAL INFORMATION:
FIGURE 1 SEQUENCE ACTOR SEQUENCE ACTOR AND POLYPEPTIDES
TITLE OF INVENTION: WOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR PILING DATE: 2000-04-18
PRIOR FILING DATE: 2001-04-16
PRIOR PELING DATE: 2001-04-16
SPRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 10994
SOFTWARE CURLOM
SEQ ID NO 8991
LENGTH: 1189
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TILE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT APPLICATION NUMBER: 90/522,929
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
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                                                                                                                                                                                                                                                                                                            Score 49; DB 1; Length 458;
Pred. No. 56;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              380 QGQNWTQGFNNYYDQGYGNYNSA 402
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Best Local Similarity 34.8%;
Matches 8; Conservative ;
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Best Local Similarity
Matches 9; Conserva
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PCT-US01-08656-8991
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Human prostate can Human prostate can FIV TALTYM4 envelo Human prostate can Renal cancer assoc Streptomyces nogal FIV UK14 envelope Translation of TEV

Mouse PAMP protein Subpeptide 4N of t Thrombospondin 1 (

Ovr115 homolog pro Human tumour suppr Human 20P1F12-GTC2 Mouse Dishevelled-

Human TMPRSS2 prot HrPCa6/7 polypepti

Human LEA-motif de FIV DUTCH6 envelop Grass pollen aller

Cell binding domai Human ORFX ORF1286

FIV UK5 envelope p Human thrombospond Human variant thro

Rat sperm coating

bcl-x(L)/bcl-2 ass bcl-x(L)/bcl-2 ass Human secreted pro Env polypeptide of FIV JAPANTM2 envel Human testis speci

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Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad; programmed cell death; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
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                                                                                                AAR51251
AAY44013
AAR51256
AAB00042
AAB74450
                                                                                                                                                                                                                                                 AAB63728
AAY07087
AAY91062
AAR58584
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AAY44406
AAY97560
AAY97550
AAY97550
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AAR97638
AAB41522
AAW61538
AAR51258
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AAR95167
AAR95165
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AAB63729
AAB63732
AAR51262
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AAY92050
                                                                 AAB64776
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                                                                                 AAR28033
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 96US-0717123
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(IDUN-) IDUN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-217267/19.
N-PSDB; AAV25877.
WO9812328-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1998
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\begin{matrix} 4 & 44 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\ 0.0 \\
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   RESULT
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Shorter murine BAD
bcl-x(L)/bcl-2 ass
Murine BCL-XL/BCL-
Mutant BCL-XL/BCL-
Mutant BCL-XL/BCL-
Mutant BCL-XL/BCL-
Mutant BCL-XL/BCL-
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Human cell prolife
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35.525 Million cell updates/sec
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                                                                                                              October 9, 2001, 15:53:27; Search time 44.37 Seconds
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**Sinssignation**

**Sinssignat
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                               412676 segs, 60623988 residues
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1 QSSSWTRVFQSWWDRNLGRGSSAPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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AAB48287
AAW32476
AAB70370
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AAW61315
AAW61316
AAW61317
AAW61318
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AAB13512
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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1145
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                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide and polypeptide sequences of proteins associated with cell proliferation for diagnosis, prevention and treatment of e.g. cancer, acquired immunodeficiency syndrome, and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cell proliferation; APOP-1; cancer; inflammation; infection; trauma; neurodegenerative disease; ischaemic injury; wasting disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                       used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
             The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-XI results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be
                                                                                                                                                                                                                                                            diseases, e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis and viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 145; DB 19;
Pred. No. 1.1e-13;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cell proliferation protein APOP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 qssswtrvfqswwdrnlgrgssapsq 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QSSSWTRVFQSWWDRNLGRGSSAPSQ
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ilarity 100.0%; P.
Conservative 0;
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                                                                                                                                                                                                                                                                                                                        detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-451230/39.
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Best Local Similarity
Matches 26; Conserv
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              atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus, emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lupus errythematosus, multiple sclerosis, mysathenia gravis, myocardial or pericardial inflammation, osteoporosis, rheumatoid arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulation, infections, trauma, disorders with associated apoptosis including AIDS and other infectious and genetic immunodeficiencies, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, ischaemic injuries such as myocardial infarction, and wasting diseases including cachexia.
adult respiratory distress syndrome, allergies, anaemia, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (I) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser118 of a human BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, nootropic, antiischaemic, vulnerary, cytostatic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCl-XL/BCl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischemenic; vulnerary; cytostatic; antiviral; antiarthritti: antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischeemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or Serl13 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated or synthetic polypeptide
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                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                 100.0%; Score 145; DB 21;
100.0%; Pred. No. 1.1e-13;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                1 OSSSWTRVFQSWWDRNLGRGSSAPSQ
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                           168 AA;
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                                                                                                                                                                                                                                                                                                   Query Match
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antiarthritic, antiinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence repersents a specifically claimed human BAD mutant amino acid sequence from the present invention.
      88888888888888888888
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168 AA; Sequence

ö Gaps ö Length 168; Indels 100.0%; Score 145; DB 22; 100.0%; Pred. No. 1.1e-13; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 26; Conservative

1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26 ò

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AAB48287 standard; protein; 168 AA. AAB48287

AAB48287;

(first entry) 02-APR-2001

Human Bad protein.

S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic.

Ношо

WO200075184-A1

14-DEC-2000

05-JUN-2000; 2000WO-US15449

99US-0137494. 04-JUN-1999;

(UYYA ) UNIV YALE.

Kondo T; Zhang H, Tsvetkov LM,

WPI; 2001-061703/07. N-PSDB; AAC84599.

Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -

Claim 5; Page 102-103; 162pp; English.

The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/ CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c.Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for treating tumours 

168 AA; Sequence

(first entry)

02-MAY-2001

ö ö The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with Bc1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo. Gaps Gaps Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bcl-2 ; ö Length 168; Length 166; Indels Indels Score 139; DB 18; Pred. No. 7.8e-13; 2; Mismatches 0; Score 145; DB 22; Pred. No. 1.1e-13; BBC6 gene; cell death; cell cycle; Bcl2; human. 100.0%; Scor. 100.0%; Pred. No. 1... 0; Mismatches BBC6 protein for regulating cell death. Claim 1; Column 11-12; 7pp; English. ¥ ¥. 1 OSSSWTRVFQSWWDRNLGRGSSAPSQ 26 1 QSSSWTRVFQSWWDRNLGRGSSAPSQ AAW32476 standard; Protein; 166 AAB70370 standard; protein; 162 96US-0665617. Query Match 95.9%; Best Local Similarity 92.3%; Matches 24; Conservative 96US-0665617 (first entry) 26; Conservative (CLON-) CLONTECH LAB INC WPI; 1997-447980/41. Query Match Best Local Similarity Matches 26; Conserv 166 AA; N-PSDB; AAT91561 Homo sapiens 18-JUN-1996; 18-JUN-1996; US5663316-A. 02-SEP-1997. 15-JAN-1998 Xudong Y; AAB70370; AAW32476; Sequence 9 RESULT AAW32476 AAB70370 RESULT ò g g XXXXXX ò

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bcl-x(L)/bcl-2 associated death promoter protein.
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(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Seril8 of a human

BAD, Seri55 of a murine BAD (longer murine BAD) or Seri13 of a murine

BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

nootropic, antischaemic, vulnerary, cytostatic, antiviral,

antiarthritic, antiinflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitior. BAD polypeptides and

polynucleotides can be used for screening candidate compounds

for activity that promote cell survival or apoptosis. Other uses include

polynucleotides can be used for screening candidate compounds

inducting or inhibiting apoptosis in a cell. Candidate compounds

identified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases. neurodegenerative diseases, ischaemic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

lymphoproliferative conditions, arthritis, infertility, inflammation and

autoimmune diseases. The present sequence represents a specifically

claimed shorter murine BAD mutant amino acid sequence from the present
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                                        immunostimulant; neuroprotective; nootropic; antischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiniflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                              Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                              New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
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Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
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Pred. No. 4.5e-10;
3; Mismatches 4;
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Best Local Similarity 73.1%;
Matches 19; Conservative
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                                                                                                                                                                Synthetic.
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06-JAN-1997 (first entry)

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Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; appototic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treat neurodegenerative diseases, immunodeficiency diseases
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                                                                                                                                                                                                                                           147..149
/note= "BH1 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                 "BH2 conserved amino acids"
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73.1%; Pred. No. 5.8e-10;
ive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                        111..130
/note= "PEST sequence"
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                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 1; 130pp; English.
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                                                                                                                                                       Mus musculus
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ID AAW6
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Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

Mutant BCL-XL/BCL-2 associated cell death regulator #1.

07-OCT-1998 (first entry)

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD protein a heterologous polypeptide that increases intracellular delibery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infection, and autoimmune disease. Polyuuclectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, adjug or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated on the specified Ser, forming a product that does not hosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promating cell survival. The mutants with
                                                                                                             Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                           Murine BCL-XL/BCL-2 associated cell death regulator.
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Pred. No. 5.8e-10;
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Best Local Similarity 73.1%;
Matches 19; Conservative
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                                     (first entry)
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N-PSDB; AAV27833.
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                                     07-0CT-1998
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AAW61315;
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis infertility, contranged inflammation and autoimmune disease. Polynucleotide sequences encoding inflammation and autoimmune disease. Polynucleotide sequences encoding contranged in a sa disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers or transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful. In treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family continued cannot bind 14-3-3.
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llarity 73.1%; Pred. No. 5.8e-10;
Conservative 3; Mismatches 4;
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                Synthetic.
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Gaps

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Length 204; 4; Indels Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

97WO-US19175

17-OCT-1997; 18-OCT-1996;

30-APR-1998.

WO9817682-A1.

Mus sp. Synthetic.

(UNIW ) UNIV WASHINGTON.

Korsmeyer SJ;

WPI; 1998-261422/23. N-PSDB; AAV27836.

Mutant BCL-XL/BCL-2 associated cell death regulator #3

07-OCT-1998 (first entry)

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death regulator) proceins, having an amino acid other than Ser at proseint in a door 15, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins of mutant BAD with reduced apoptosis, e.g. cancer, viral infection, lymphoptoliferation, arthritis; infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful
                                                          Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In treatment of excessive proptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have prosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Scr substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                          New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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Pred. No. 5.8e-10;
3; Mismatches 4; Indels 0
                                   BCL-XL/BCL-2 associated cell death regulator #2.
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Best Local Similarity 73.1%;
Matches 19; Conservative
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          07-OCT-1998 (first entry)
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N-PSDB; AAV27835.
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                                                                                                  Mus sp.
Synthetic.
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                                   Mutant
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New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection

Claim 7; Page 60-61; 95pp; English.

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at obsition 112 and/or 136, relative to the murine BAD 24 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility infertility
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Ser substituted cannot bind 14-3-3.
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Pred. No. 5.8e-10;
3; Mismatches 4; Indels 0
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73.1%;
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nes 19; Conservative
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Matches
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1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26

AAW61318 standard; Protein; 204 AA.

RESULT 11 AAW61318 AAW61318;

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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a novel serine-phosphorylated protein, BAD (Rel-2) associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator. Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, senescence, neurodegenerative disease, ischaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
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immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
                                                           BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator
                                                                                                immunodeficiency disease; neurodegenerative disease; infertility;
cancer, viral infection; lymphoproliferative condition; arthritis;
inflammation; autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                               polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 120; DB 19;
Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB70369 standard; protein; 204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QSSSWTRVFQSWWDRNLGRGSSAPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               э;
Э;
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 8; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.8%;
                                                                                                                                                                                                                          97WO-US15871.
                                                                                                                                                                                                                                                 96US-0707868
          23-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                          (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                          WPI; 1998-207049/18.
                                   Murine BAD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    Korsmeyer SJ;
                                                                                                                                                                          WO9809643-A1
                                                                                                                                                                                                                        09-SEP-1997;
                                                                                                                                                                                                                                                  09-SEP-1996;
                                                                                                                                                                                                12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB70369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a mino acid substitutions at Serl18 of a human

(E) Ecl-XL/Bcl-2 associated cell death requiator polypeptide (BAD) or its

(E) fragment, which contains amino acid substitutions at Serl18 of a human

(E) BAD, Serl55 of a murine BAD (longer murine BAD) or Serl13 of a murine

(E) BAD, (Shorter murine BAD) (I) has immunostimilant, neuroprotective,

(E) notropic, antilachaemic, vulnerary, cytostatic, antiviral,

(E) antiarthritic, antilnflammatory and immunosuppressive activities, and

(E) can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

(E) plynucleotides can be used for screening candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell. Candidate compounds

(I) inducing or inhibiting apoptosis in a cell.

(I) candidate compounds

(I) inducing or inhibiting apoptosis in a cell.

(I) inducing or inhibiting apoptosis in a cell.

(I) inducing or inhibiting apoptosis in a cell.

(I) inducing inducing inducing a cell infamination and autoimmune diseases. The present amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;
cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Serl18, Serl55 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bcl-x(L)/bcl-2 associated death promoter epitope, residues 182-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%; Score 120; DB 22; 73.1%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 148; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR95167 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000; 2000WO-US11864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-138734/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200110888-A1:
                                                                                                                                                                                                                                                                                                                     Mus musculus.
Synthetic.
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The sequences given in AAR95155-67 represent epitopes derived from the murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see also AAR95168). Bad is a 22.1 KD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-c related family clustered in the BH1 and BH2 domain. Bad has been found to hyporatidise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death countering the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L). Bad may be used to treat an european activity diseases, immunodeficiency diseases, e.g. Albs,
  The sequences given in AAR95155-67 represent epitopes derived from the murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see also AAR95168). Bad is a 22.1 KD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-crelated family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death countering the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L). Carbit which inhibit its binding to bcl-x(L). In the countering pents may be used to treat an enrodes of the countering interaction and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to treat an enrodes of the counter 
polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter-useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-x(L) to form heteromultimers
                                                        neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 103; 130pp; English.
                                                                                                                                                                                                                                                                                     95WO-US14246
                                                                                                                                                                                                                                                                                                                                              94US-0333565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 senescence or ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                      UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-251465/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 AA;
                                                                                                                                                                                                                                                                                     31-OCT-1995;
                                                                                                                                                                                                                                                                                                                                              31-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korsmeyer SJ;
                                                                                                                 Mus musculus
                                                                                                                                                                    WO9613614-A1
                                                                                                                                                                                                                            09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-z or bcl-x(L) to form heteromultimers

95WO-US14246. 94US-0333565

31-OCT-1995; 31-OCT-1994;

09-MAY-1996.

(UNIW ) UNIV WASHINGTON

WPI; 1996-251465/25

Korsmeyer SJ;

Claim 2; Page 103; 130pp; English.

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Gaps
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0
 Length 16;
55.9%; Score 81; DB 17; Length 16
75.0%; Pred. No. 1.7e-05;
iive 2; Mismatches 2; Indels
                                                                                                                                                   9, 2001, 15:53:28
 Query Match 55.9
Best Local Similarity 75.0
Matches 12; Conservative
                                                                          2 SSSWTRVFQSWWDRNL 17
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Gaps

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Score 84; DB 17; Length 16; Pred. No. 6.1e-06; 2; Mismatches 1; Indels

57.9%; 80.0%;

Query Match 57.9 Best Local Similarity 80.0 Matches 12; Conservative

5 WTRVFQSWWDRNLGR 19 |||: |||||||: | 2 wtriigswwdrnlgk 16

ŏ g Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BHI; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.

WO9613614-A1 Mus musculus

bcl-x(L)/bcl-2 associated death promoter epitope, residues 180-195.

AAR95165 standard; peptide; 16 AA.

15

AAR95165 RESULT

03-JAN-1997 (first entry)

AAR95165;

senescence or ischaemia.

16 AA;

Sequence

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RESULT 2
BAD_MOUSE
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cavia porce
moraxella b
bacillus st
poa pratens
                                                                                                                                                9, 2001, 15:55:21; Search time 17.79 Seconds (without alignments) 50.064 Million cell updates/sec
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Q61337 mus musculu
P55472 rhizobium s
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rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mus musculu
rattus norv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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P55472

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P10502

P105
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          93435 segs, 34255486 residues
                                                                                                                                                                                                                                                                                                                       QSSSWTRVFQSWWDRNLGRGSSAPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                  US-09-580-523-1_COPY_143_168
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POLG_BCMVN
POLG_LMV0
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TMS2_HUMAN
LPH_RABIT
DVL1_MOUSE
DVL1_RAT
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TPX1_CAVPO
MTM2_MORBO
YMA3_BACST
MP91_POAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAD_MOUSE
NOEE_RHISN
CRS3_HUMAN
POLG_PEMVC
CTPI_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENV_FIVT2
TPX1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSP1_BOVIN
TSP1_HUMAN
TSP1_MOUSE
POLG_PVYHU
POLG_PVYN
MAUG_METME
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                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLG_LMVE
                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length
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419
419
245
3068
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Perfect score:
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Perret X.;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Brain, and Thymus;
MEDLINE-95186361; PubMed=7834748;
MEDLINE-95186361; PubMed=7834748;
MEDLINE-95186361; PubMed=7834748;
MEDLINE-95186361; PubMed=7834748;
MEDLINE-95186361; PubMed=7834748;
MEDLINE-95186361; MEDMETIC Partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
Cell 80:285-291(1995).
                                                                                                                                                                                                                                        -I-FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE BINDING TO BCL-X(L) AND BCL-2. THEREBY AFFECTING THE LEVEL HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
-I-SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH BAX, MCL-1, Al, OR BCL-X(S).
-I-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-I-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97361801; PubMed-9218762;
Hanin M., Jabbouri S., Quesada-Vincens S., Freiberg C., Perret X.,
Broughton W.J., Fellay R.;
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 1; Le
Pred. No. 3.3e-10;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOEE_RHISN STANDARD, PRT; 419 AA. P55472; P72326; 01-NOV-1997 (Rel. 35, Created) 115-DEC-1998 (Rel. 35, Last sequence update) 115-DEC-1998 (Rel. 37, Last annotation update) NODULATION PROTEIN NOEE (EC 2.8.2.-).
                         (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                         BAD PROTEIN (BCL-2 BINDING COMPONENT 6) BAD OR BBC6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 QSAGWTRIIQSWWDRNLGKGGSTPSQ 204
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.8%;
Best Local Similarity 73.1%;
Matches 19; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1096330; Bad
                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 1
182 1
204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOEE OR Y4HB.
                          01-NOV-1997
                                     01-NOV-1997
                                                   01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis.
 BAD_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYSTEINE-RICH SECRETORY PROTEIN-3 PRECURSOR (CRISP-3) (SGP28 PROTEIN).
'Sulphation of Rhizobium sp. NGR234 Nod factors is dependent on noeE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDILINE-96270732; PubMed-8665901;
KRIATINE-96270732; PubMed-8665901;
Donner D., Schleuning W.-D.;
The human cysteiner-rich secretory protein (CRISP) family. Primary structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
Eur. J. Blochem. 236:827-836(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
MEDLINE-96186934; PubMed-8601434;
Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
"SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with similarity to a human testis-specific gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFIC GRANULES.
-!- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >
EPIDIDYMIS, OVARY, THYMUS AND COLON.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                    MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and a rodent sperm-coating glycoprotein.";
FEBS Lett. 380:246-250(1996).
-!- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
                                                                                                                                                                                                                                                                    "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-!- FUNCTION: REQUIRED FOR THE FORMATION OF SULFATED NOD FACTOR
PROPOSED TO TRANSFER ACTIVATED SULFATE (PAPS) TO THE FUCOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%; Score 65; DB 1; Length 419; 47.6%; Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: LIMITED TO NODH AND TO C.ELEGANS F42G9.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46569 MW; 848C48E0416AAA1F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                   a new host-specificity gene.";
Mol. Microbiol. 24:1119-1129(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000076; AAB91690.1; -. Nodulation; Transferase; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3_HUMAN STANGE
CRS3 HUMAN STANGE
101-0CT-1996 (Rel. 34, Last seque
01-0CT-1996 (Rel. 34, Last seque
01-0CT-1996 (Rel. 40, Last annot
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308 YRRVFQTWWDLRRGEGEGIPA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 WTRVFQSWWDRNLGRGSSAPS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y09415; CAA70569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         THE NOD FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 AA;
                                                                                                       [2]
SEQUENCE FROM N.A.
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Last sequence update)
15-DEC-1993 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (FORTAINS: W-TERMINAL PROTEIN (P1); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (C1); 6 KDA PROTEIN 2 (6K2);
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
(EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
COAT PROTEIN (CP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE-33033110; Pubmed-1413501;
Wance V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.;
"The complete nucleotide sequence of pepper mottle virus genomic RNA: comparison of the encoded polyprotein with those of other sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pepper mottle virus (California isolate) (PemV) (PepMoV C).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                          CYSTEINE RICH SECRETORY PROTEIN-3.
N-LINKED (GLCNAC. .) (POTENTIAL).
S -> P (IN REF. 2).
B4DD79CB7AE9E5F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL PROTEINS.
SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
SIMILARITY: N-A PROPEINASE BELONGS TO PEPTIDASE FAMILY C4.
SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 1; Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3068 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                               Pfam; PFUULBS; SCF. T. PRINTS; PROBB37; VSTPLIKE.
PROSITE; PSO1009; SCP_AGS_PRI_SC7_1; 1.
PROSITE; PSO1010; SCP_AGS_PRI_SC7_2; 1.
Glycoprotein; Signal; Multigene family.
20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 SSSWSQAIQSWFDEYNDFDFGVGPKTPN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SSSWTRVFQSWWDR----NLGRGSSAPS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
                                                                                                                                           EMBL; X95240; CAA64527.1; -. EMBL; X94323; CAA63984.1; -. HSSP; P04284; 1CFE. InterPro; IPR01283; -. Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                               245 AA; 27630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              39.3%;
39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=31737;
                                                                                                                                                                                                                                                                                                              21
239
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLG_PEMVC
Q01500;
                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase; Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase; ATP-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KDA PROTEIN 1.
CYTOPLASMIC INCLUSION PROTEIN.
6 KDA PROTEIN 2.
GENOME-LINKED PROTEIN.
NUCLEAR INCLUSION PROTEIN A.
NUCLEAR INCLUSION PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 1; Length 3068;
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COAT PROTEIN.
COVALENT LINKAGE OF VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               HELPER COMPONENT PROTEINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1248 ATP (POTENTIAL).
AA; 348651 MW; FD3458BB37FDA7C2 CRC64;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROBABLE CATION-TRANSPORTING ATPASE I (EC 3.6.1.-).
CTPI OR RV0107C OR MICY251.26C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN P3
                                                                                                                                                                                                                                                                                                                    Pfam; PF0057; Poty_1; 1.
Pfam; PF00767; Poty_coat; 1.
Pfam; PF007680; RNA_dep_RNA_pol; 1.
Pfam; PF000271; helicase_C; 1.
PRINTS; PR00966; NIAPOTYPTASE.
                                                                                                                                                                                                                                                                                            PF00863; Peptidase_C4; 1. PF00851; Peptidase_C6; 1.
                                                                                                                    EMBL; M96425; AAA46903.1; -.
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50.0%;
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1191 FESWWDEQVARGFTIP 1206
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Best Local Similarity 50.0v
                                                                                                                                                                                      InterPro; IPR001205; ...
InterPro; IPR001410; ...
InterPro; IPR001456; ...
InterPro; IPR001592; ...
InterPro; IPR00150; ...
InterPro; IPR00150; ...
InterPro; IPR00130; ...
InterPro; IPR00240; ...
Pfam; PF00270; DEAD; 1.
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2795
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743
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MEROPS; C04.001; -.
MEROPS; C06.001; -.
MEROPS; S30.001; -.
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InterPro; IPR001410;
InterPro; IPR001456;
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1906
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Q10900;
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SEQUENCE
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BINDING
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Pfam;
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Pfam; PF00271;
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       Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Harry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moules S., Murphy L., A. Oliver S., Seeger K., Skelton S., Squres S., Squres T., Skelton S., Squres S., Squres T., Skelton S., Squres S., Squres T., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Rutter S., Seeger K., Skelton S., Squares S., Squres T., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Rutter S., Seeger K., Skelton S., Squares S., Squres T., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Lociphering the biology of Mycobacterium tuberculosis from the complete genome sequence.;

Later Sais31-34(1999)

C. I. CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.

C. I. STMLLARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY

(El-E2 ATPASES). STRONGEST SIMILARITY TO EUKARYOTIC CALCIUM-TRANSPORT SYSTEMS.
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: W-TERMINE: W-FOUTEIN (Pl); HELPER
COMPONENT PROTEINASE (EC 3.4.22..) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                Tuberculist; Rv0107c; -., InterPro; IPR000695; -. InterPro; IPR001757; -. InterPro; IPR001899; -. PRm; SP00122; B1-E2_ATPase; I. PRINTS; PR00119; CATATPASE. PRINTS; PR00120; HATPASE.
                                                                                                                                                                                                                                                                                                                                                     EMBL; 274410; CAA98940.1; -.
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71.48;
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1576 WDRSPGRASSAPRQ 1589
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1567
1053
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Best Local Similarity
Matches 10; Conserv
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ID POLG_TUMVJ
AC P89509;
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SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on its
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-1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
MAY BE INVOLVED IN REPLICATION.

-1- FUNCTION: UNCLEAR INCLUSION PROTEIN A HAS PROTECLYTIC ACTIVITY.

-1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

-1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

-1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

-1- PTM: THE VYBAL RNA OF POTYVIRUSES IS EXPRESED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTECLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTECLY.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=3707908; PubMed=8920830; MEDLINE=37077908; PubMed=8920830; Obshina K., Tanga M., Sako N.; "The complete nucleotide sequence of turnip mosaic virus RNA Japanese "The complete nucleotide sequence
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA) (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)}.
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                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6. SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4 SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY
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Pred. No. 12;
3; Mismatches 7; Indels
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CYTOPKARMIC INLUSION PROTEIN.
6 KDA PROTEIN 2.
GENOME-LINKED PROTEIN.
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W; ODFC735CB3A5231F CRC64;
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                                                                                                                       Turnip mosaic virus (strain Japanese) (TuMV)
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RNA_dep_RNA_pol; 1.
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Pfam; PF00863; Peptidase_C4; 1.
Pfam; PF00851; Peptidase_C6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001456; -. InterPro; IPR001592; -.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                   Potyvirus.
NCBI_TaxID=12230;
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Pfam; PF00767;
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Pfam; PF00767; Poty_coat; 1.
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Q02282;
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                                                                                                       01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
6ENOME POLYPROTEIN [CONTAINS: N'TERMINAL PROTEIN (Pl); HELPER
COMPONENT PROTEINAE (EC 3.4.22.-) (HC-PRO); PROTEIN P3: 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (Cl); 6 KDA PROTEIN 2 (6K2);
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
(EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
                                                                                                                                                                                                                                                                                                                                             MEDLINE-93057350; Pubmed-1431807; Nicolas O, Laliberte J.F.; "I"The complete nucleotide sequence of turnip mosaic potyvirus RNA."; J. Gen. Virol. 73:2785-2793(1992).
                                                                                                                                                                                                                                                                                                                              Iremblay M.F., Nicolas O., Sinha R., Lazure C., Laliberte J.F.;
"Sequence of the 3'-terminal region of turnip mosaic virus RNA and
                                                                                                                                                                                              Turnip mosaic virus (strain Quebec) (TuMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1534-3163 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-91073142; Pubmed-2254757;
                                                                            PRT; 3163 AA
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                                                                                               01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D10927; BAA01725.1; -. EMBL; D10601; BAA01452.1; -. PIR; JQ1168; JQ1895.
                   : | |||: | || : |
1261 KTFASWWNHQLSRGFTIP 1278
         7 RVFQSWWDRNLGRGSSAP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IPRO01410; ...; IPRO01456; ...
                                                                             STANDARD;
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Pfam; PF00863; Peptidas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001205;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=36396;
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MEROPS; C06.001;
                                                                           POLG_TUMVQ
002597;
                                                                                                                                                                                                                   Potyvirus.
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                                                                  POLG_TUMVQ
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ENV POLYPROTEIN PRECURSOR (GP150 POLYPROTEIN) (CONTAINS: GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachi A.;
"Identification of feline immunodeficiency virus rev gene activity.";
J. Virol. 65:4539-4542(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Pfam; PF00680; RNA_dep_RNA_pol; 1.
PRINTS; PR00966; NIAPOTYPTASE.
Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase; Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92198230; PubMed=1312825;
Maki N., Miyazawa T., Fukasawa M., Hasegawa A., Hayami M., Miki K.,
Mikami T.;
                                                                                                                                                                                                                                                                                                                                                    COVALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kiyomasu T., Miyazawa T., Furuya T., Shibata R., Sakai H.,
Sakuragi J.I., Fukasawa M., Maki N., Hasegawa A., Mikami T.,
                                                                                                                                                                                      6 KDA PROTEIN 1.
CYTOPLASMIC INCLUSION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 3163;
                                                                                                                                                                                                                                                                                      A.B
                                                                                                                                             HELPER COMPONENT PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                          G (IN REF. 2). 61B0F73B58DF6D59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular characterization and heterogeneity of feline
                                                                                                                                                                                                                                                                                    NUCLEAR INCLUSION PROTEIN NUCLEAR INCLUSION PROTEIN
                                                                                                                                                                                                                                    6 KDA PROTEIN 2.
GENOME-LINKED PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feline immunodeficiency virus (isolate TM2) (FIV).
                                                                                                                        N-TERMINAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB Pred. No. 17; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                 COAT PROTEIN.
                                                                                                                                                                     PROTEIN P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency virus isolates.";
Arch. Virol. 123:29-45(1992).
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Pfam; PF00429; ENV_polyprotein; 1.
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1261 KTFASWWSHOLSRGFTIP 1278
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44.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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1870
1923
2115
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2875
3163
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Best Local Similarity
8; Conserve
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2359
2876
1986
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InterPro; IPR001283; -.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
PRSt1s; Signal; Multigene family.
SIGNAL.
                                                                                                                                                                                                                                                                                             105 TSWSSAIQSWYDEILDFVYGVGPKSPN 131
                                                                                                                                                                                                                                                                            3 SSWTRVFQSWWDRNL----GRGSSAPS 25
                                                                                                                                                                                                                27259 MW;
                                                                                                                                                                                                                                          34.5%;
37.0%;
                                                                                                       EMBL; M25532; AAA61220.1; -. EMBL; X95239; CAA64526.1; -.
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.08
Matches 10, Conservative
                                                                                                                        PIR; B33329; B33329.
MIM; 187430; -.
                                                                                                                                                                                                                 243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                          (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (CYSTEINE-RICH SECRETORY
                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                  Score 51; DB 1; Length 855; 
Pred. No. 8.6; 
0; Mismatches 7; Indels
Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                           BC2DFABB6245D70D CRC64;
          GLYCOPROTEIN GP100
                                N-LINKED (GLCNAC.
         MAJOR GLYCOPROTEIN
GLYCOPROTEIN GP36.
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MEDLINE-90129048; PubMed-2613236;
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                                                                                                                                                                                                                                                                                    35.2%;
56.2%;
Coat protein; Polyprotein;
                                                                                                                                                                                                                                                           98238
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Best Local Similarity 50.2
The 9; Conservative
                                                                                                                                                                                                                                                                                                                                        383 QSGSWIRTISSWKQRN 398
                                                                                                                                                                                                                                                                                                                      1 QSSSWTRVFQSWWDRN 16
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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4499
5318
531
551
720
728
736
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                                                                                                                                                                                                                                                         855 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                 TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                  TPX1_HUMAN
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CARBOHYD
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TPX1_HUMAN
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-!- TISSUE SPECIFICITY: TESTIS AND EPIDIDYMIS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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Mammalla; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HOLSTEIN; TISSUE=Tooth;
MEDLINE-98173773; PubMed-9507054;
Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoue H.; "cDNA cloning of bovine thrombospondin 1 and its expression in odontoblasts and predentin."; Biochim. Biophys. Acta 1382:17-22(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TESTIS-SPECIFIC PROTEIN TPX-1.; C5FE698C449CFAD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 1; Length 243;
Pred. No. 3.4;
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la Fleur M., Jobin C., Gauthier J., Kreis C.G.;
Submitted (Xxx.1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ADHESTVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRONECTIN,
   1030 QSSSRFYVVMWKQVTQSYWDTN 1051
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                                                                                                  TSP1_HUMAN
P07996;
                                                                                                                                                                                                                                                                                                                                                                                          proteins
                                                                                  TSP1_HUMAN
                                                                   RESULT
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and also as its content is no way modified and this statement is not removed. Usage by and for commercial
                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TSP TYPE-1 1.

TSP TYPE-1 2.

TSP TYPE-1 3.

EGF-LIKE 1.

EGF-LIKE 2.

TSP TYPE-3 1.

TSP TYPE-3 2.

TSP TYPE-3 3.

TSP TYPE-3 5.

TSP TYPE-3 6.

TSP TYPE-3 6.

TSP TYPE-3 6.

TSP TYPE-3 6.

TSP TYPE-3 7.

CTELMINAL.

CELL ATTACHMENT SITE (POTENTIAL).
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Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
EGF-like domain; Signal.
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 !- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
!- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
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PROSITE; PS00022; ESF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01208; VWRC; 1.
                                                                                                                                                                            EMBL; AB005287; BAA21115.1; -.
                                                                                                                                                                                             EMBL; X87618; CAA60950.1; -. EMBL; X87619; CAA60951.1; -.
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Pfam; PF00090; tsp_1; 3.
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TISSUE=Endothelial cells;
MEDLINE=87057617; PubMed=2430973;
Lawler J., Hynes R.O.;
"The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologies with several different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-397 FROM N.A.
MEDLIND-87157592; PubMed=3030396;
Kobayashi S., Eden-Mccutchan F., Framson P., Bornstein P.;
"Partial amino acid sequence of human thrombospondin as determined by analysis of CDNA clones: homology to malarial circumsporozoite proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-374 FROM N.A.
MEDLINE-86287276; PubMed-3461443;
Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
"Characterization of a cDNA encoding the heparin and collagen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,
Baumgartel D.M., Rotwein P., Frazier W.A.;
"Complete thrombospondin mRNA sequence includes potential regulatory
sites in the 3' untranslated region.";
J. Cell Biol. 108:729-736(1989).
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"Chharacterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription."; J. Biol. Chem. 264:11222-11227(1989).
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domains of human thrombospondin.";
Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
THROMBOSPONDIN 1 PRECURSOR.
1170 AA
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MEDLINE=89139590; Pubmed=2918029;
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STANDARD;
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                                                                                                                                                                                                                                                    (Human)
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Gaps

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Indels

Score 50; DB 1; Length 1170;

Pred. No. 16;

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Conservative

Query Match Best Local Similarity Matches 11; Conserv

34.5%; 50.0%;

BONDS

1030 QSSSRFYVVMWKQVTQSYWDTN 1051

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          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01092; TSP1; 3.
PROSITE; PS01208; VWFC; 1.
Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat; EGF-like domain; Signal.
  as its content is in no
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-> A (IN REF. 2).
69B3EDE5AE3A395E CRC64;
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N-LINKED (GLCNAC. . .) (P
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EGF-LIKE 1.
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                                                     EMBL; M25631; AAA36741.1; -. EMBL; X04665; CAA28370.1; -.
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InterPro; IPR000884; -.
InterPro; IPR001007; -.
Pfam; PF00008; EGF; 2.
Pfam; PF00093; vwc; 1.
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PIR; A25812; A25812.
PIR; A26155; A26155.
PIR; A30140; A30140.
PIR; A34274; A34274
HSSP; P35555; IEMO.
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MEDLINE-90375546; PubMed=2398070;

Bornstein P., Alfi D., Devarayalu S., Framson P., Li P.;

Gharacterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";

J. Biol. Chem. 265:16691-16698(1990).

-I- FUNCTION: ADHESTVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND.

CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRONECTIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of mouse thrombospondin 2 sequence and expression
                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-92147683; Pubmed=1371115;
Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92128941; PubMed=1774063;
Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert
Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
-:- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-:- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-:- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
-:- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
-:- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of the murine thrombospondin gene."; Genomics 11:587-600(1991).
                                                                                                           Last sequence update)
Last annotation update)
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                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
                                                                                                                                                               THROMBOSPONDIN 1 PRECURSOR
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                      (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M62458;
M62459;
M62460;
                                                                                                                                                                                           THBS1 OR TSP1
                                                                                                     01-JUN-1994
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dixit V.M.;
                        TSP1 MOUSE
P35441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
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EMBL;
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EMBL;
EMBL;
EMBL;
TSP1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                 HIDDRY REPRESENTED DESCRIPTION OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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50.0%;
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Best Local Similarity 50.0
Matches 11; Conservative
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AAA50611.1;

M62464;

1 QSSS-----WIRVFQSWWDRN 16

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3061 AA

PRT;

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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
6ENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (Pl); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN CRO);
6ENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
COAT PROTEIN (CP)].
POCATO VILUS Y (Strain Hungarian) (PVY).
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=93154578. PubMed=8428653;
Thole V., Dalmay T., Burgyan J., Balazs E.;
"Cloning and sequencing of potato virus Y (Hungarian isolate) genomic
           STANDARD;
                                                                                                                                          Potyvirus.
NCBI_TaxID=31739;
          POLG_PVYHU
Q02963;
                                                                                                                                                                                                         RNA.";
            1;
                                                                                                                                                                                                                                                                     TSP TYPE-1 1.
TSP TYPE-1 1.
TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 3.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 6.
TSP TYPE-3 7.
                                                                                                                            InterPro; IPR000884; -.
InterPro; IPR001007; -.
Ffam; PF00009; EGF; 2.
Pfam; PF00090; tSp_1; 3.
PROSITE; PS01086; EGF_1; FALSE_NEG.
PROSITE; PS01086; EGF_2; 1.
PROSITE; PS01086; EGF_2; 1.
PROSITE; PS01086; EGF_2; 1.
PROSITE; PS01086; EGF_2; 1.
PROSITE; PS01089; VWFC; 1.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF_1ike domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%; Score 50; DB 1; Length 1170; 50.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                      HEPARIN-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> L (IN AAA53063).
0443E493615E7F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
N-LINED (GLCNAC. . ) (F
                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
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THROMBOSPONDIN 1.
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F -> L (I)
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                         EMBL; M62468; AAA50611.1; JOINED.
EMBL; M62469; AAA50611.1; JOINED.
EMBL; M62469; AAA50631.1; JOINED.
EMBL; J05606; AAA40431.1; -
EMBL; J05605; AAA40431.1; -
PIR; A40558; A40558.
PIR; A45587; B42587.
PIR; A47905; A37905.
                  JOINED.
JOINED.
JOINED.
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          M62466; AAA50611.1;
M62467; AAA50611.1;
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                                                                                                           MGD; MGI:98737; Thbs1.
InterPro; IPR000561; -.
InterPro; IPR000884; -.
InterPro; IPR001007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1067 106
1025 102
1170 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase; Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-TERMINAL PROTEIN.
HELPER COMPONENT PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDA PROTEIN 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01577; Poty_P1; 1.
Pfam; PF00767; Poty_coat; 1.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00270; DEAD; 1.
Pfam; PF00863; Peptidase_C4; 1.
Pfam; PF00851; Peptidase_C6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIGH; FF00Z/1; DELICASE_C; 1.
PRINTS; PR00966; NIAPOTYPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M95491; AAB59762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001205; InterPro; IPR001410; InterPro; IPR001456; InterPro; IPR001592; InterPro; IPR001509; InterPro; IPR001530; InterPro; IPR001730;
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824
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MEROPS; C04.001; -.
MEROPS; C06.001; -.
MEROPS; S30.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002540;
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276
825
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1 QSSS-----WTRVFQSWWDRN 16

us-09-580-523-1\_copy\_143\_168.rsp

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EMBL; X12456; CAA30988.1;
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                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 34, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: N TERMINAL PROTEIN (PI); HELPER
COMPONENT PROTEINS: N TERMINAL PROTEIN P3; 6 KDA PROTEIN
1 (KAL), CYTOPLASHIC INCLUGION PROTEIN (CI); 6 KDA PROTEIN 2
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN 8 (NI-A) (NI-A)
(EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
COAT PROTEIN (CP)].
PROTEIN (CP)].
VICUSES: SSRNA POSITIVE-STRAND VILUSES; NO DNA STAGE; POLYVITIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Durand Tardif M.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
-!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY.
-!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
-!- FUNTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
-!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
-!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST BIGHT
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robaglia C., Durand-Tardif M., Tronchet M., Boudazin G., Astier-Manifacier S., Casse-Delbart F.; "Nucleotide sequence of potato virus Y (N Strain) genomic RNA."; J. Gen. Virol. 70:935-947(1989).
                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                   POLG_PVYN STANDARD; PRT; 3063 AA.
P18247; Q85266; Q85267; Q85269; Q85270; Q85271; Q85272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i-SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
-i-SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
-i-SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                        COAT PROTEIN.
COVALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).
                                                                                                                                                                                Score 50; DB 1; Length 3061;
Pred. No. 43;
2; Mismatches 7; Indels
 CYTOPLASMIC INCLUSION PROTEIN.
                                            NUCLEAR INCLUSION PROTEIN A. NUCLEAR INCLUSION PROTEIN B.
                                                                                                                      ATP (POTENTIAL).
MW; 737FFBA215B56F99 CRC64;
               6 KDA PROTEIN 2.
GENOME-LINKED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89279275; PubMed=2732709;
                                                                                                                                                                               Query Match 34.5%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                    347326
                                                                                                                                                                                                                                                              | |||| : | : |
1192 FSDWWDRQIQMGHTLP 1207
                                                                                                                                                                                                                                            9 FQSWWDRNLGRGSSAP 24
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                                          2275
2794
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3061 AA;
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                                                        2276
2795
1907
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SEQUENCE
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POLG_PVYN
CHAIN
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Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COAT PROTEIN.
COVALENT LINKAGE OF VIRAL RNA (BY
                                                                                                                                                                                                                                                                                                                                                                                          6 KDA PROTEIN 1.
CYTOPLASMIC INCLUSION PROTEIN.
6 KDA PROTEIN 2.
GENOME-LINKED PROTEIN.
NUCLEAR INCLUSION PROTEIN A.
NUCLEAR INCLUSION PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 3063; 43;
                                                                                                                                                                                                                                                                                                                                                                  HELPER COMPONENT, PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
W; 3EC79125DE33F1BB CRC64;
                                                                                                                                                                                                                                                                                                                                                    N-TERMINAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 1
Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                         PF00680; RNA_dep_RNA_pol; 1.
PF00271; helicase_C; 1.
                                                                                                                                                                                                Peptidase_C4; 1.
                                                                                                                                                                                                                 Peptidase_C6; 1.
                                                                                                                                                                                                                                                                        Pfam; PF00271; helicase_C; 1.
PRINTS; PR00966; NIAPOTYPTASE.
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\\; 347535 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.5%;
43.8%;
EMBL; D00441; BAA00342.1;
PIR; JS0166; JS0166.
MEROPS; C04.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 43.5-
Local 7; Conservative
                                                                                                                                                                                                                                              _coat;
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                                                                                                                      InterPro; IPR001592; -. InterPro; IPR001650; -.
                                                                                                                                                    InterPro; IPR001730; -.
InterPro; IPR002540; -.
                                                                                                                                                                                                                                                                                                                                                                                                             1791
1843
                                                                                                                                                                              Pfam; PF00270; DEAD; 1
                                                                                                                                                                                                                                                                                                                                                                                               157
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                                                                      InterPro; IPR001205;
InterPro; IPR001410;
                                                                                                         InterPro; IPR001456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3063 AA;
                                            MEROPS; C06.001; -.
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1907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2276
                                                          MEROPS; S30.001
                                                                                                                                                                                              Pfam; PF00863;
Pfam; PF00851;
                                                                                                                                                                                                                                                            Pfam; PF00680;
                                                                                                                                                                                                                              Pfam; PF01577;
                                                                                                                                                                                                                                            PF00767;
                                                                                                                                                                                                                                                                                                                                   ATP-binding.
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BINDING
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9, 2001, 15:55:22 Search completed: October Job time: 197 sec

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us-09-580-523-1.rpr

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version	- 2000
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OM protein - protein search, using sw model

October 9, 2001, 15:50:10; Search time 28.81 Seconds (Without alignments) 444.197 Million cell updates/sec Run on:

US-09-580-523-1 905 1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

1: piri:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

													:																
Description	bad protein - mous	hypothetical prote	Ξ	probable immediate	hypothetical prote		chromogranin B pre	Ħ	omega-conotoxin-se	chromogranin A pre	RNB6 protein - rat	serine-rich protei	SNF2beta protein -	eyelid - fruit fly	hypothetical prote	homeotic protein H	hypothetical prote	LFY floral meriste	filaggrin - mouse	endozepine related	vasodilator-stimul	hypothetical prote	pHL E1F1 - human	hypothetical prote	ಹ	hypothetical prote		u	filaggrin precurso
ID	A55671	T42702	T18396	T03166	T30757	A35938	S15901	T45115	A42566	A41520	JC5614	A44067	S45252	T13049	T43500	WJMS13	T05221	B38104	A31488	T49431	S51797	T00329	154810	T24786	I38465	T00037	T29146	WJHUIC	A28444
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% Query Match Length	204	834	1729	1300	336	2248	646	2237	2339	449	393	1077	1647	2715	222	270	343	420	254	337	380	1095	134	380	1159	1323	1562	270	313
% Query Match	711.7	10.5	10.3	10.3	10.2	10.1	6.6	6.6	6.6	9.6	٠			9.6			•	9.5	4.6	4.6	9.4	9.4	9.3	9.3	9.3	9.3	9.3	6.3	9.3
Score	649	95	93.5	93	92.5	91.5	90	90	90	89.5	88.5	86.5	86.5	86.5	86	98	98		85.5	82	82	85	4	4	84.5	84.5	<u>.</u>	84	84
Result No.		7	æ	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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hypothetical prote	zyxin - chicken	hypothetical prote	polycomb protein e	profilaggrin - rat	tracheal colonizat	myosin-IA - Acanth	probable transcrip	trithorax protein	enkephalin e-12 pr	EH domain protein	hypothetical prote	probable secretory	heterogeneous ribo	nucleolin homolog	hypothetical prote
S16506	A44358	807132	T13154	A34615	140333	T32734	T51947	A35085	EQBOA	T09173	T16726	T36677	A33616	T09648	T02858
N	N	7	~	7	N	7	7	7	-	~	~	~	7	7	7
381	542	988	2023	625	672	1215	1392	3759	263	743	160	523	558	635	751
9.3	9.3	9.3	9.3	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.1
84 9.3	84 9.3	84 9.3	84 9.3	83.5 9.2	83.5 9.2	83.5 9.2	83.5 9.2	83.5 9.2	83 9.2	83 9.2	83 9.2	82.5 9.1	82.5 9.1	82.5 9.1	82.5 9.1

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C; Species: Mus musculus (house mouse)
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C; Argang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A; Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A; Reference number: A55671; MUID: 95136361
A; Accession: A55671
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-204 < YAN>
A; Residues: 1-204 < YAN>
A; Cross-references: GB:L37296; NID:g639778; PIDN: AAA64465.1; PID:g639779
C; Keywords: heterodimer
bad protein - mouse
```

3; 61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMŚDE 120 98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 157 Gaps 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQOEQPTSSSH 60 9 Query Match 71.7%; Score 649; DB 2; Length 204; Best Local Similarity 75.6%; Pred. No. 2.1e-45; Matches 127; Conservative 12; Mismatches 23; Indels ð g δλ

121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168 158 FEGSF-KGLPRPKSAGTATOMROSAGWTRIIQSWWDRNLGKGGSTPSQ 204 q ò q

1

RESULT '2

742702

Nalicaral protein DKFZp434F117.1 - human (fragment)

Nalicarate names: hypothetical protein DKFZp434B239.1

Nalicarate names: hypothetical protein DKFZp434B239.1

C. Species: Homo sapiens (man)

C. Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 02-Jun-2000

C. Accession: 742702; 746602

N. Reference number: 222334

A. Reference number: 222334

A. Reference number: 222334

A. Reference in RNA

A. References: EMBL: AL133028

A. Status: preliminary

A. Molecule type: mRNA

A. Residues: 1-834 < AAA>

A. Cross references: EMBL: AL133028

A. Experimental source: adult testis; clone DKFZp434F117

R. Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

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probable immediate early protein - alcelaphine herpesvirus 1
C.Species: alcelaphine herpesvirus 1
C.Species: alcelaphine herpesvirus 1
C.Species: alcelaphine herpesvirus 1
C.Accession: T03166
R.Ensser, A.: Pflanz, R.: Fleckenstein, B.
A. Virol. 71, 6517-6525, 1997
A.Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A.Reference number: 214840; MUID:97404659
A.Accession: T03166
A.Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 155R - Molluscum contagiosum virus 1
N.Alternate names: MC15R
C.Species: MOlluscum contagiosum virus 1
C.Species: Molluscum 130757
R.Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816. 1996
A.Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host A; Reference number: 220876; MUID:96325459
A; Reference number: 220876; MUID:96325459
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-336 <SEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PEFEPSEQEDSSSAERGLGP-SPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 2; Length 1300;
Pred. No. 8.3;
6; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AGAVEIRSRHSSYPAGTEDDEGMGEE------PSPFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 2.1;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92.5;
Pred. No. 2.
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30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.3%;
Best Local Similarity 29.0%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  profilaggrin - human (fragments)
C;Species: Homo sapiens (man)
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Best Local Similarity 30.00
The 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Plasmodium falciparum) (!ragm C; Species: Plasmodium falciparum) (!ragm C; Species: Plasmodium falciparum) (| Species: Plasmodium falciparum (| Species: Plasmodium falciparum) (| Species: Plasmodium fals) (| Species: Preliminary: | Lanslated from GB/EMBL/DDBJ |
| A; Residuas: | L-1729 | CBAR | | |
| A; Residuas: | L-1729 | CBAR |
| A; Residuas: | L-1729 | CBAR |
| A; Residuas: | RMBL: U27339; | NID: 9914920; | PID: 9914921; | PIDN: AAA89134.1 |
| A; Note: var-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erythrocyte membrane protein variant 2 – malaria parasite (Plasmodium falciparum) (fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       983 AGATGLQL-----PGVTVDD----SDPDPQTQLKRGNIPNDFLRQMFYTLGDYRDICI 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 RSKILKNAESDPRSSERDQLRPGDESTPRGRCDSRGNQRKTPPVNAKFSIMPAWQKFSDG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSR----HSSYPAGTEDDE-GMGEEPSP----FRGRSRSAPP----NLWAAQRY--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GRELRRMSDEFVDSFKK-----GLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPPAGV--------RELGK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 PSGNESSPSEKLPQGPTPETTKETPESSLLHAFVSPPRLRRFLPW---HKFKEQWKAQHG 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRY------ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDSSSAERGLGPSP---AGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 834;
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submitted to the Protein Sequence Database, January 2000 A; Reference number: 223029
                                                       A) Accession: T46502
A) Status: preliminary
A; Molecule type: mRNA
A; Residues: 213-834 <AA2>
A; Cross-references: EMBL: AL137336
A; Cross-references: eMBL: AL137336
A; Stoperimental source: adult testis; clone DKFZp434B239
A; Note: DKFZp434F117.1; DKFZp434B239.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.5%; Score 95; DB 3 Best Local Similarity 27.6%; Pred. No. 3.5; Matches 50; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.3%; Score 93.5; D
Best Local Similarity 21.6%; Pred. No. 10;
Matches 42; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G 373
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S21773; MUID:92207983
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                               S21773
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        A;Reference n
A;Accession:
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A;Residues: 567-580 <FLA>
R;Dillen, L. Boel, S.; de Potter, W.P.; Claeys, M.
Biochime, Biophys. Acta 1120, 105-112, 1992
A;Title: Mass spectrometric characterization of bovine chromaffin granule peptides relat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; MCGCULE type: mRNA
A; Residues: 1-646 <BIO.
A; Cross-references: EMBL:X55027; NID:g11; PIDN:CAA38846.1; PID:g12
A; Grandy, D.K.; Leduc, R.; Makam, H.; Flanagan, T.; Diliberto, E.J.; Thomas, G.; Civelli
submitted to the EMBL Data Library, October 1990
A; Description: Nucleotide and deduced amino acid sequence of bovine adrenal medulla Chrc
A; Reference number: $20727
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A; Residues: 21-63, N', 65-92, FRS', 96, FRA', 99-100, 'S', 101-480, 'L', 482-646 <GRA>
A; Residues: 21-63, N', 65-92, FRS', 96, FRA', 99-100, 'S', 101-480, 'L', 482-646 <GRA>
A; Cross-references: EMBL: NS 201; PIDN:CAA39109.1; PID:9202
B; Flanagan, T.: Taylor, L.; Poulter, L.; Viveros, O.H.; Diliberto Jr., E.J.
Cell. Mol. Neurobiol. 10, 507-523, 1990
A; Title: A novel 1745-Dalton pyroglutamyl peptide derived from chromogranin B is in the A; Reference number: A61076; MUID:91223542
                      C;Accession: A35938
R;Gan, S.Q.; McBride, O.W.; Idler, W.W.; Markova, N.; Steinert, P.M.
Biochemistry 29, 432-9440, 1990
A;Title: Organization, structure, and polymorphisms of the human profilaggrin gene. A;Reference number: A35938; MUID:91064347
A;Stecession: A35938
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S15901; S20727; A61076; S21773; S39369
R;Bauer, J.W.; Fischer-Colbrie, R.
Biochim. Biophys. Acta 1089, 124-126, 1991
A;Title: Primary structure of bovine chromogranin B deduced from cDNA sequence. A;Reference number: S15901; MUID:91223091
C; Date: 14-Dec-1990 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 SQSVAGQRQARSRHQSHQEST------RGRSRG-----GSGRSGSFLYQVST 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQEDSSSAER-GLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGG----- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2248;
                                                                                                                                                                                                              A.Molecule type: DNA
A.Residues: 1-2248 <GAN>
A.Residues: 1-2248 <GAN>
A.Cross-references: GB:J02929
C.Genetics:
A.Gene: GDB:FLG
A.Cross-references: GB:119912; OMIM:135940
A.Map position: 1q21-1q21
C.Superfamily: unassigned calmodulin-related proteins; calmodul: C.Superfamily: unassigned calmodulin-repeat
F.246-569/Region: filaggrin repeat
F.570-893/Region: filaggrin repeat
F:1074-1397/Region: filaggrin repeat
F:1573-1896/Region: filaggrin repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EFVDSFKKGLPRPKSAGTATQMRQSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 HEQSESSHGWAR----TSTGRRQGS 273
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Best Local Similarity
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Matches
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A; Residues: 567-580 Coll.>
B; Yoo, S.H.
B; Yoo, S.H.
B; Yook S.H.
B; Yook S.H.
B; Yook S.H.
A; Title: pH-dependent binding of chromogranin B and secretory vesicle matrix proteins
A; Reference number: S39369; MUID: 94032431
A; Residues: 239-244; 565-555 < xoo>
C; Superfamily: chromogranin B precursor
C; Keywords: adrenal gland; glycoprotein; pituitary; pyroglutamic acid; sulfoprotein
C; Keywords: adrenal gland; glycoprotein; pituitary; pyroglutamic acid; sulfoprotein
C; Keywords: adrenal gland; glycoprotein; pituitary; pyroglutamic acid; sulfoprotein
F; 1-20/Comain: signal sequence #status predicted AMAT>
F; 567-580/Product: chromogranin B #status predicted AMAT>
F; 567-580/Product: chromogranin B #status predicted
F; 36-57/Disulfide bonds: #status predicted
F; 315/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 315/Binding site: sulfate (Tyr) (covalent) #status predicted
F; 315/Binding site: sulfate (Tyr) (covalent) #status predicted
F; 567/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
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C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45115
R;Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; Science 257, 389-395, 1992
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-A; Reference number: A4256; MUID:92335886
A;Accession: T45115
A;Accession: T45115
A;Accession: T45115
A;Accession: T45115
A;Accession: T45115
A;Reference number: A256; MUID:9235886
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2337 < WILL>
A;Residues: 1-2337 < WILL>
A;Residues: CCHIA2
C;Genetics: CCHIA2
C;Genetics: CCHIA2
C;Function: A;Description: calcium influx
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 PGESEEDA-----SPEVDKRHSRPRHHGRSRP----DRSSQEGNPPLEEESHVGTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 NSDEEKARHPAHFRALEEGAEYGEEVR--RHSAAQAPGDLQGARFGGRGRGEHQALRRPS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SHQQEQPTSSSHHGGAGAV-EIRSRHSSYP-AGTEDDEGMGEEPS-PFRGRSRSAP 101
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28.7%; Pred. No. 6.8;
iive 16; Mismatches
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A; Wolecule type: protein
A; Residues: 19-34, X', 36-38; 97-111; 134-139 <BA2>
A; Residues: 19-34, X', 36-38; 97-111; 134-139 <BA2>
R; Watkinson, A.; Joensson, A.C.; Davison, M.; Young, J.; Lee, C.M.; Moore, S.; Dockra Biochem. J. 276, 471-479, 1991
A; Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and A; Reference number: $15847; MUID:91264803
A; Accession: $15847
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A;Molecule type: mRNA
A;Residues: 1-135,'S',137-190,'Y',192-253,'P',255-310,'H',312-318,'K',320-390,'Q',392
A;Cross-references: EMBL:X04012; NID:g197; PIDN:CAA27636.1; PID:g198
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FEBS Lett. 334, 373-377, 1993
A;Title: Nature of the pH-induced conformational changes and exposure of the C-termin
A;Reference number: S38976; MUID:94063061
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A;Accession: 146008
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A;Residues: 19-26;266-272 <YOO>
C;Comment: Chromogranin A is the major protein of bovine chromaggin granules.
C;Comment: Chromostatin activity has been demonstrated from proteolytic fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 210, 14', 312-318, K', 320-331 < MA2>
A; Note: 311-Arg and 319-Glu were also found
B; Watkinson, A.; Rogers, M.; Dockray, G.J.
Biochem. J. 295, 649-654, 1993
A; Title: Post-translational processing of chromogranin A: differential distribution
A; Reference number: S39016; MUID:94059013
A; Accession: S39016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 303-313 - KMAT>
K;Benedum, U.M.; Baeuerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.;
EMBO J. 5, 1495-1502, 1986
                                                                                                                                                              posttranslational modifications in secretory granules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 EFEPSEQE---DSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:142-161/Product: chromostatin #status predicted <MAT3>
F:266-312/Product: pancreastatin #status experimental <MAT2>
F:35-56/Disulfide bonds: #status predicted
A; Molecule type: protein
A; Residues: 266-312 <NAK.
R; Barbosa, J.A.; Gill, B.M.; Takiyyuddin, M.A.; O'Connor,
Endocrinology 128, 174-190, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: phosphoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-449/Product: chromogranin A #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 WEEAEREKAVPEEESPPTAAFKAPPSLGNKETQRAAPGW 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 -EFVDSFKKGLPR------PKSAGTATQMRQSSSW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatches
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                                                                                                                                                              A;Title: Chromogranin A: posttranslational A;Reference number: A61114; MUID:91099142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.44
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S38976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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NACOMALINE AND AMERICAL SECRETORY Protein I; secretory protein I
N.Contains: chromostatin; pancreastatin
C.Speceles: Bos primigenius taurus (cattle)
C.Spate: 10-Sep-1999 sequence_revision 10-Sep-1999 stext_change 18-Aug-2000
C.Accession: AA1520, AA2175; A63035; A4175; A6306; A61114; S15847; S39016; 146008; S38976
R.Incangelo, A.L.: Grimes M. Eiden, L.E.
A.Ticle: The bowine chromogranin A gene: structural basis for hormone regulation and generate chumber: A41520; MUID:9214039; PhDN:AB21297.1; PID:924424
A.Morecule type: DNA
A.Rossidues: 1-449 clac>
A.Constreferences: GB:79270; NID:9244423; PIDN:AB21297.1; PID:924424
B.Ahn, T.G.: Cohn, D.V.; Gorr, S.D.; Corristin, D.L.; Kashdan, M.A.; Levine, M.A.
A.Title: Primary structure of bowine pituitary secretory protein I (chromogranin A) dedu
A.Reference number: A28033
A.Moriecule type: mRRA
A.Rossidues: 1-11, TV., 13-190, TV., 192-253, PP., 255-378, RP.
A.Rocssidues: 1-11, TV., 13-190, TV., 192-253, PP., 255-378, RP.
A.Rocssidues: LII, TV., 11-11, TV., 11-1
                                                                                                                                                                                   C; Species: Homo sapiens (main)
C; Species: Homo sapiens (main)
C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C; Accession: A42566
R; Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC
Science 257, 389-395, 1992
A; Title: Structure and functional expression of an omega-conotoxin-sensitive human N-typ
A; Reference number: A42566; MUID:9235886
A; Accession: A42566
A; Accession: A42566
A; Residues: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-2339 cWIL>
A; Residues: 1-2339 cWIL>
A; Residues: carracted from NCBI backbone (NCBIP:109168)
C; Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                          omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively splic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 EPSEQED----SSSAERGLGPSPA-----GDGPSGSGKHHRQAPGLLWDA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 2339;
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.9%; Score 90; DB 30.8%; Pred. No. 27; Live 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 36; Conserv
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Matches
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45;

57;

Length 449;

DB 1;

<MAT>

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RESULT 13

S4525

SNF2beta protein - human
C;Species: Homo sapiens (man)
C;Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
R;Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994
A;Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila br
A;Reference number: 845251; MUID:94268902
A;Reference revision: 845252
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1647 - CHI>
A;Rosidues: 1-1647 - CHI>
A;Cross-references: GB:D26156; NID:9505087; PIDN:BAA05143.1; PID:9505088
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
F;1485-1540/Domain: bromodomain homology < BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eyelid - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13049
R;Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
Submitted to the EMBL Data Library, March 1998
A;Reference number: 217592
A;Accession: T13049
A;Reference number: 217592
A;Accession: T13049
A;Reference number: 217592
A;Accession: T13049
A;Reference number: 21750
A;Coss-references: EMBL:AF053091; NID:92981220; PID:92981221; PIDN:AAC06254.1
C;Genetics:
A;Genetics:
A;Consc.references: FlyBase:FBgn0003013
C;Function:
A;Description: could act as a transcription factor antagonistic to the Wg pathway
C;Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as a transcription factor antagonistic to the Wg pathway
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                                                                                                                                                                                              73 HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRP 132
                                                                                                                                                                                                                               ----HSMYQPSSSSYPRAL----LTSP 721
                             Gaps
                                                                                   15 SSSAERGLGPSPAGDGPSG--SGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH---RQAP-GLLWDASHQQEQPTSSSHIJGGA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 PSPGPSPGSAHSMMGPSP---GPPSAG--HPIPTQGPGGYPQDNMHQMHKPMESMHEKGM 84
                             27;
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                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDDPRYNQMKGMGMRSGGHAGMGPPPSPMDQHSQGYPSPLGGSE 128
                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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Pred. No. 36;
9; Mismatches
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Best Local Similarity 25.8%; Pred. No. 61;
Matches 41; Conservative 11; Mismatches
Best Local Similarity 28.9%; Pred. No. 22; Matches 37; Conservative 17; Mismatches
                                                                                                                                  678 SSSSSG---KKCGDHPAAIISNVHHPQ----
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ilarity 29.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                            133 KSAGTATO 140
                                                                                                                                                                                                                                                                                                                                                                     773 STSGSASQ 780
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T13049
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                                               C; Species: Rattus norvegicus (Norway rat)
C; Date: 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change 05-Nov-1999
C; Accession: JC5614
C; Accession: JC5614
C; Accession: JC5614
C; Accession: JC5614
Biochem. Biophys. Res. Commun. 237, 307-312, 1997
A; Title: Differential display cloning of a novel rat cDNA (RNB6) that shows high express A; Accession: JC5614; MUID: 97415794
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                  A; MOJECULE type: mRNA
A; Residues: 1-393 <OHT>
A; Residues: 1-393 <OHT>
A; Cross-references: GB:U70211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462
A; Experimental source: brain
C; Comment: This protein belongs to Ena/VASP family member, and is involved in the develo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Bang, A.G.; Posakon, J.W.
Genes Dev. 6, 1752-1769, 1992
A;Title: The Drosophila gene Hairless encodes a novel basic protein that controls altern
A;Reference number: A44067; MUID:92387549
A;Accession: A44067
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A;Residues: 1-1077 <PRE>
A;Cross-references: BMBL:X67239; GB:S49642; NID:g578331; PID:g578332
B;Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
Mech. Dev. 38, 143-156, 1992
A;Title: Hairless, a Drosophila gene involved in neural development, encodes a novel, A;Reference number: S33412; MUID:93041287
A;Accession: S33412; MUID:93041287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library, May 1994
Drosophila gene involved in neural development, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: Ī-150,'A',152-701,'LL',704-890,'R',892-963,'RLLP',968-973,975-1077 <MAI>A;Cross-references: EMBL:X67239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serine-rich protein hairless - fruit fly (Drosophila melanogaster)
N'Alternate names: 109K basic protein H
C'Species: Drosophila melanogaster
C'Species: Drosophila melanogaster
C'Date: 10-Jun-1993 *sequence_revision 26-Feb-1999 *text_change 26-Feb-1999
C'Accession: A44067; A58929; S33412; S24639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 ------HSSYPAGTEDDEGMGEEP--SPFRG-RSRSAPPNLWAAQRYGRELRRMSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 LLAKRRKAASQTDKPADRKEDENQTEDPSTSPSPGSRATSQPPNSSEAGRKFWERSNSVE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Wolecule type: DNA
A;Residues: 19-1077 <BAN>
A;Cross-references: GB:W95192; NID:q157621; PID:q157622
A;Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)
R;Preiss, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 EDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQOEQPTSSSHHGGAGAVEIRSR 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.8%; Score 88.5; Dr
Best Local Similarity 28.2%; Pred. No. 5.2;
Matches 40; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 KPVSSL---LSRVKPAGSVNDV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 EFVDSFKKGLPRPKSAGTATOM 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
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                          protein - rat
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A,Gene: FlyE
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Tue Oct

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C; Accession: T43500
R; Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, December 1999
A; Reference number: 222515
A; Reference number: 222515
A; Accession: T43500
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-22 cAAA>
A; Cross-references: EMBL:AL133642
A; Experimental source: adult uterus; clone DKFZp586G1721
C; Genetics:
A; Note: DKFZp586G1721.1
                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKF2p586G1721.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                         56 --TSSSHHGGAGAVEIRSRHSSYPAGT-EDDEGMGEE------PSPFRGRSRSAPPNL 104
                                                                                                                   73 ------HSSYPAGTEDDEGMGEEP--SPFRG-RSRSAPPNLWAAQRYGRELRRMSD 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 EDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
8 EPSEQEDSSSAERGLG-PSPAGDGPSGSGKHHRQAPG-----LLWDASHQQEQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 9.5%; Score 86; DB 2; Length 222; Best Local Similarity 27.3%; Pred. No. 4.4; Matches 41; Conservative 15; Mismatches 56; Indels
                                                                                                                                                                                                    105 WAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQ 143
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Search completed: October 9, 2001, 15:54:03 Job time: 233 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2001, 15:52:05; Search time 17.79 Seconds Run on:

(without alignments) 323.492 Million cell updates/sec

US-09-580-523-1 905 1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Q61337 mus musculu	000555 homo sapien		P23389 bos taurus	Q00975 homo sapien	P11675 pseudorabie	P05059 bos taurus		m	P51532 homo sapien	P09021 mus musculu	096013 homo sapien	2 homo	homo	mus m	Q69154 murine cyto	homo	homo	gallu	~	5 mus m	P20659 drosophila	P01211 bos taurus	9	-	80	10	'n	004933 craterostig		_	P23771 homo sapien
SUMMARIES	ID	BAD_HUMAN	BAD_MOUSE	CCAA_HUMAN	CYAA_NEUCR		CCAB_HUMAN	IE18_PRVIF	CMGA_BOVIN	DMP1_BOVIN	HLES_DROME	SN24_HUMAN	HXA5_MOUSE	PAK4_HUMAN	VASP_HUMAN	Y553_HUMAN	ST13_MOUSE	IE63_MCMVS	HERG_HUMAN	HXA5_HUMAN	ZYX_CHICK	ARVC_HUMAN	NKCR_MOUSE		PENK_BOVIN	ROL_HUMAN	CCT_DROME	FILA_MOUSE	LFY_ARATH .	MANA_RHOMR	SPS2_CRAPL	Z174_HUMAN	NKC1_SQUAC	GAT3_HUMAN
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	Query Match	82.2	71.7	10.7				6.6					9.5		4.6		9.3	٠	9.3	9.3	9.3	9.3	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.0	9.0	
	Score	744	649	97	94.5	90	90	89.5	88.5	88.5			98	98	82	æ	•	84.5	٠	84	84	æ	83.5	83.5	α	82.5	ď	82	82	82	82	81.5	4	81
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Gaps

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Query Match 82.2%; Score 744; DB 1; Length 168; Best Local Similarity 85.1%; Pred. No. 1e-49; Matches 143; Conservative 0; Mismatches 25; .Indels

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CYAA_PODAN  CYAA_PODAN  CO1513 podospora a P5112 fugu rubrip P52D_BOVIN  P58D_BOVIN  P58T_BOVIN  P58T_	ALIGNMENTS RT; 168 AA.	updat n upo 6). 2a; V	Zhou H.; enBank/Daba databas SUCCESSFULLY COMPE THEREBY AFFECTING SE PROTEINS WITH BA ELL-X(L), BUT NOT TH BCL-X(L), AND BCL Y SIMILARITY). OMOLOGY DOMAIN 1 (B OMOLOGY DOMAIN 2 (B	is produced through a commatics and the EMBL. There are no restrict ong as its content is ved. Usage by and follows the follows is sufficient to the follows of the follows its produced by the follow
CYAA- HD_FL PSPD- VE2_F FYB_F CABL- 5E5_F IE18- IE18- IRFL	ALIO PRT;	ted) sec	Chen S. e EMBL/G L DEATH, D BCL-2, BOTH THE TIVITY O TIMERS WI -X(S) (B PRESSED PRESSED PRESSED PRESSED THE BCL-2 H	OT entry is copyright. It Swiss Institute of Bioinfe Bioinformatics Institutions as profit institutions as tatement is not remulates a license agreement (ail to license@isb.sib.ch).  AAB36516.1;  AAB36516.1;  01 121 BH1.  46 163 BH2.  8 AA; 18408 MW; BDF3D999
2145 3148 369 369 7802 12220 12230 1244 1244 1244 1244 1244 1244 1244 124	ARD;	(Rel. 35, Created) (Rel. 35, Last seq (Rel. 40, Last and (BCL-2 BINDING COM BCL2L8. (Human) theria; Primates; 606;	ENCE FROM N.A.  D.X., Li Z., Huang B., Ci the (NOV-1996) to the function: PROMOTES CELL BINDING TO BCL-X(L) AND HETERODIMERIZATION OF BY SIMULARITY: FORMS HETERODI BAX, MCL-1, A1, OR BCL-TISSUE SPECIFICITY: EXPISIONES SIMILARITY: CONTAINS A SIMILARITY: CONTAINS A SIMILARITY: BELONGS TO	ry is copy Institute Ormatics I institut tatement i license a license(i license(i) licen
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		_ α X ⊐ σ	Li Z. Huad (NOV-1996) (NOV-1996) (NOV-1996) (NOV-1996) (NOV-1996) (NOT-1996)	SWISS-PROT- ten the Swill uropean Bio by non-pro lied and thin lies require and an email U66879; AA 603167; - AA N 146 N 146 N 146 N 146
881 880.5 880.5 880.5 80.5 79.5 79.5 79.5 79.5	ULT 1 _HUMAN BAD_HUMAN		YIN D.X., Li Z., Huang Submitted (Nov1996) to Submitted (Nov1996) to -!- FUNCTION: PROMOTES BINDING TO BCL-X(L HETERODIMERIZATION THE DEATH REPRESSOI (BY SIMILARITY). -!- SUBUNIT: FORMS HETY BAX, MCL-1, Al, OR BAX, MCL-1, Al, OR -!- TISSUE SPECIFICITY -!- SIMILARITY: CONTAII.	This SWISS-PROT entry is coppetween the Swiss Institute the European Bioinformatics use by non-profit institutenties requires a license or send an email to license or sen
	RESULT BAD_HU ID B		2	

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Q92690; Q16290; Q99790; Q99791; Q99792; Q99793; P78510;
                                                                                                                                                                                                                                                                                                          TISSUE=Cerebellum;
                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    channel.
                                                                                     (BI)
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                                                                                                                                                                                                                                         TISSUB-Brain, and Thymus;

TISSUB-Brain, and Thymus;

TISSUB-Brain, and Thymus;

MEDLINE-95136361; PubMed-7834748;

Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;

"Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";

Cell Boi.285-291(1955).

-!-FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE BINDING TO BCL-X(L) AND BCL-2, THERRBY AFFECTING THE LEVEL HETERODIMERIZATION OF BOTH THESE PROFEINS WITH BAX. CAN REVERSE THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.

-!-SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L), AND BCL-2, BUT NOT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 204;
                     BAX, MCL-1, A1, OR BCL-X(S).
-!- SIMILARITY: CONTAINS A BCL-2 HOWOLGGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOWOLGGY DOMAIN 2 (BH2).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
           FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 649; DB 1; 75.6%; Pred. No. 1.7e-42; ive 12; Mismatches 23;
                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
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Best Local Similarity 75.65
Matches 127; Conservative
                                                                                               STANDARD;
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                                                                                                                                                                                   Mus musculus (Mouse).
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204 AA;
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                                                                                                                                                                       BAD OR BBC6.
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                                                                                               BAD_MOUSE
Q61337;
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CCAA_HUMAN
ID CCAA_HU
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                                                                                  BAD_MOUSE
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT PVO_TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97053792; PubMed=8898206; Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J., Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J., Hoffman S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E., Lindhout D., van Ommen G.-J.B., Hofker M.H., Ferrari M.D., Frants R.R.; "Femilial hemiplegic migraine and episodic ataxia type-2 are caused by mutations in the Ca2+ channel gene CACNLIA4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOMET. CELI MOI. GENET. 21:279-284(1995).

-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED ENTRY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A GIVES RISE TO P AND/OR O'TYPE CALCIUM CURRENTS. PA'O-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E., McInnis M.G., Ross C.A.; "Characterization of cDNA clones containing CCA trinucleotide repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Neuron;
MEDILTRE=991518614; PubMed=10049321;
MEDILTRE=99158614; PubMed=10049321;
Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
Harpold M.M., Johnson E.C., Williams M.E.;
"Structural elements in domain IV that influence biophysical and
pharmacological properties of human alphalA-containing
high-voltage-activated calcium channels.";
Biophys. J. 76:1384-1400(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJNE-97141920; PubMed-8988170; Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W., Annos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.; "Autosomal dominant cerebellar ataxia (SCA6) associated with small polyglutamine expansions in the alpha 1A-voltage-dependent calcium
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MEDLINE=95123449; PubMed=7823133;
MEDLINE=951203449; PubMed=7823133;
MEDLINE=9512000 M.P., Kim Y.I., Froehner S.C.;
"Expression and antibody inhibition of P-type calcium channels in human small-cell lung carcinoma cells.";
J. Neurosci. 15:274-283(1995).
                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2)
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                    CACNAIA OR CACNLIA4 OR CACH4 OR CACN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2038-2258 FROM N.A. TISSUE=Frontal cortex; MEDLINE=96102310; PubMed=8525433;
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PRINTS; PR00167; CACHANNEL

IN A 1:1:11 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORDER FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BY DIRECTED BY THE PROBLET ALPHA-1 SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALCHA-2/DELTA .

-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1. ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; BI-1/1A-2, BI-1(V1), BI-1-GCCAG/1A-1 (SHOWN HERE), BI-1/(Y1)-GGCAG, BI-1/(Y2)-GGCAG/1A-1 (SHOWN HERE), BI-1/(Y1)-GGCAG, BI-1(V2), BI-1(V2)-GCCAG/1A-1 (SHOWN HERE), BI-1-GCCAGAG, BI-1(V2), BI-1(V2)-GGCAG AND BI-1(V2)-V3); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1. TISSUE SPECIFICITY: BRAIN-SPECIFIC; MAINLY FOUND IN CEREBELLUM, CEREBRAL CORTEX, THALAMUS AND HYPOTHALAMUS. NO EXPRESSION IN HEART, KIDNEY, LIVER OR MUSCLE: PREXIMILY FOUND IN CEREBELLAR GORDER, CONTAIN TO CREBEBLILAR GRANULE CELLS.

-1. DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SECHENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SECHENTS (S1, S2, S3, S5, S6) AND SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION:

-1. POLYMORPHISM: THE POLY CAIN RECION OF CAONAIA IS POLYMORPHIZE: 6 TO INTERPRATE IN STINOCERBELLAR ATRAIRA 6 (SCAG) PATENTS: THERE SEEMS THE NEARMED THE REPEAT IN SHINOCERBELLAR ATRAIRA 6 (SCAG) PATENTS: THERE SEEMS THE NEORDED TO ABOUT 21 TO 30

REPEATS IN SHINOCERBELLAR THE REPEAT NUMBER AND EALLER ONSET OF COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS

DISEASE: EXPANSION OF A CAG REPEAT IN THE CODING REGION OF CACNAIA IS THE CAUSE OF ONE FORM OF SPINOCEREBELLAR ATAXIA 6 (SCA6), AN AUTOSOMAL DOMININT DISORDER CHARACTERIZED BY SLOWLY PROGRESSIVE CEREBELLAR ATAXIA OF THE LIMBS AND GAIT, DYSAFTHRIA, NYSTAGWIS, AND MILD VIBRATORY AND PROPRIOCEPTIVE SENSORY LOSS. THESE SYMPTOMS ARE PROBABLY EXPLAINED BY SEVERE LOSS OF CEREBELLAR PURKINJE DISORDER. THE

DISEASE: DEFECTS IN CACNAIA ARE THE CAUSE OF FAMILIAL HEMIPLEGIC MIGRAINE (FHM), ALSO KNOWN AS MIGRAINE FAMILIAL HEMIPLEGIC 1 (MHPI), EDISODIC ATAXIA TYPE 2 (EA-2), ACETAZOLAMIDE RESPONSIVE COMMUN TYPES OF MIGRAINES. FHM, A RARE AUTOSOMAL DOMINANT SUBTYPE OF MIGRAINE WITH ARRA, IS ASSOCIATED WITH ICTAL HEMIPARESIS AND, IN SOME FAMILLES, PROGRESSIVE CERBEBLLAR ATROPHY. EA-2 IS ANOTHER AUTOSOMAL DOMINANT PROXYSMAL CEREBRAL DISEASE, CHARACTERIZED BY ACETOZOLAMIDE-RESPONSIVE ATTACKS OF CEREBELLAR ATAXIA AND MIGRAINE. LIKE SYMPTOMS, INTERICTAL NYSTAGMUS, AND CEREBELLAR

SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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AAB49675.1; ALT\_INIT.
AAB49676.1; ALT\_INIT.
AAB49677.1; ALT\_INIT.
AAB49678.1; ALT\_INIT. X99897; CAA68172.1; -280114; :: NOT\_ANNOTATED\_CDS. 280115; :: NOT\_ANNOTATED\_CDS. U79666; AAB64179.1; -AAB49674.1; ALT\_INIT. EMBL; AF004884; AAB61613.1; -. EMBL; AF004883; AAB61612.1; -. U79668; **U79665** U79667 EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; 

-; NOT\_ANNOTATED\_CDS Pfam; PF00520; ion\_trans; 4. InterPro; IPR000636; -. 006702; S76537 EMBL; EMBL;

Calcium channel, Glycoprotein, Repeat, Multigene family, Calcium-binding, Phosphorylation, Alternative splicing; Polymorphism; Disease mutation, Triplet repeat expansion. Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; S4 OF REPEAT II (POTENTIAL).
SY OF REPEAT II (POTENTIAL).
SS OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SS OF REPEAT II (POTENTIAL).
SS OF REPEAT II (POTENTIAL).
SI OF REPEAT III (POTENTIAL).
SY OF REPEAT III (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
SY OF REPEAT III (POTENTIAL). EXTRACELLULAR (POTENTIAL). S4 OF REPEAT III (POTENTIAL). CYTOPLASMIC (POTENTIAL). S5 OF REPEAT III (POTENTIAL). EXTRACELLULAR (POTENTIAL). S6 OF REPEAT III (POTENTIAL) OF REPEAT IV (POTENTIAL). FOPLASMIC (POTENTIAL). SZ OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). S1 OF REPEAT IV (POTENTIAL). EXTRACELULAR (POTENTIAL).
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2373 PARSESPRACRHGGARWPASGPHVSEGPPGPRHHG------YYRGSDYDEADG 2419 2420 PGSGGGEEAMAGAYDAPPPVRHASSGATGRSPRTPRASGPACASPSRHG---RRLPNGYY 2476 ----PSPFR----GRS----RSAPPNLWAAQRYGRELRRMSDEFV 122 ----GLLWDAS--HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE------GMGEE---43 82 ò g õ g

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                                                                                                                                                                                                                                                                                                                                                                                    Kore-Eda S., Murayama T., Uno I.; "Isolation and characterization of the adenylate cyclase structural
                                                                                                                    01-JUL-1993 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
ADENYLATE CYCLASE (EC. 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                          gene of Neurospora crassa.";
Jpn. J. Genet. 66:317-334(1991).
-!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
-i- SIMILARITY: BELONGS TO ADENIYIL CYCLASE CLASS-3 FAMILY.
-i- SIMILARITY: COWPAINS 23 LEUCINE-RICH REPEATS (LRR).
-i- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
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Prámn; PPO0481; PP2C; 1.
PRINTS; PRON019; LEURINFT.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
LYASE; Repeat; Leucine_rich repeat; CAMP synthesis; Magnesium.
                                                                                                                                                                                                                                            Neurospora crassa.
Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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                                                                                CYAA_NEUCR
Q01631;
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Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolytin, the endogenous C-terminal fragment of residues 614-626 with antibacterial activity.";

Eur. J. Biochem. 229:356-368(1995).
                                                                                                                                                          Gaps
                                                                                                                                                                                                          EIRSRHSS----YPA----GTEDDEGMGEEP----SPFRGR--SRSA 100
                                                                                                                                                                                                                                          400 GGRDRDASPVPSRPRIPVPAPEVVPFLYQEADDIARYGEAPVRTSLTGPDRDRYIDSSQN 459
                                                                                                                                       17 SAERGLGPSPAGDGPSGSGKHHR ---- QAPGLLWDASHQQEQPTSSSHH-----GGAGAV 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovidae; Bovidae; Bovidae; McBL_TaxID=9913;
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1. 40, Last annotation update)
PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Adrenal chromaffin;
MEDLINE=91223091; PubMed=2025642;
Bauer J.W., Fischer-Colbrie R.;
"Primary structure of bovine chromogranin B deduced from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J., Thomas G., Civelli O., Viveros O.H.; Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                                                                     Length 2300;
                                                                                                     74; Indels
221 POLY-GLN.
254752 MW; 52E79B90E6B17A7B CRC64;
                                                                                                                                                                                                                                                                            PPNLWAAQRYGREL - - - - - - - RRMSDEFVDSFKKGLPRPKSAGT - - - -
                                                                   10.4%; Score 94.5; DB 1; 24.2%; Pred. No. 9.7; iive 23; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1089:124-126(1991).
                                                                                                                                                                                                                                                                                                                                              140 QMRQSS---SWTRVFQSWWDRNLGRGSSAPS 167
                                                                                                                                                                                                                                                                                                                                                                            520 RSRAQSPAPSWTGTSRGLKANSISDGTSSPA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Adrenal chromaffin;
MEDLINE=95262699; PubMed=7744058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Adrenal medulla;
MEDLINE-97282588; PubMed-9136897;
                                                                                                                                                                                                                                                                                                                                                                                                                                               chromogranin B.";
FEBS Lett. 406:259-262(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 21-646 FROM N.A. TISSUE=Adrenal medulla;
                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECRETOGRANIN I PRECURS
PEPTIDE; SECRETOLYTIN]
                 2300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoo S.H., Kang Y.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 634-646.
                                                                                     Similarity
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2339 AA

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                          FUNCTION: SECRETOCRAIN I IS A NEUROENDOCRINE SECRETORY GRANULE PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BYOLOGICALLY ACTIVE PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.
FUNCTION: SECRETOLYTIN HAS ANTIBACTERIAL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGR-----ELRRMS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH--RQAPGLLWDASHQQEQP--TSSSHHGGA 64
                                                                                                                                     PTM: O-GLYCOSYLATED (PROBABLE). SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
        MEDLINE=96184581; PubMed=8603705;
Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;
Antibacterial activity of secretolytin, a chromogranin B-derived
Peptide (614-656), is correlated with peptide structure.";
FEBS Lett. 379:273-278(1996).
                                                                                                                  SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                               GAWK PEPPIDE.
SECRETOLYTIN.
BY SIMILARITY.
SULFATATION (POTENTIAL).
SULFATATION (BY SIMILARITY).
N -> S (IN REF. 1).
N -> D (IN REF. 2).
SEAPGL -> FRSPRAS (IN REF. 3).
H -> R (IN REF. 2).
H -> R (IN REF. 2).
H -> R (IN REF. 2).
M -> N (IN REF. 3).
M -> V (IN REF. 3).
M -> V (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Indels
                                                                                                                                                                                                                                                                                                                                                                     Sulfatation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                           SECRETOGRANIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.9%; Scot.
28.7%; Pred. No. 5...
... 16; Mismatches
CHARACTERIZATION OF SECRETOLYTIN.
                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0659; CHROMOGRANIN.
PROSITE; PSO0422; GRANINS_1; 1.
PROSITE; PSO0423; GRANINS_2; 1.
                                                                                                                                                                                                                                                              EMBL; X55027; CAA38846.1; -. EMBL; U88551; AAC48720.1; -. EMBL; X55489; CAA39109.1; -. PIR; S15901; S15901.
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Best Local Similarity
Matches 37; Conserv
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REAL TISSUE=LUNG fibroblast;

RIA TISSUE=LUNG fibroblast;

RIA L.S. JUNG H.H., PATK S.H., Chin H.;

RIA L.S. JUNG H.H., PATK S.H., Chin H.;

RIA D.S. JUNG H.H., PATK S.H., Chin H.;

SUBMITTEG (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: VOLPAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE EMBLY OF CALCIUM TONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED

CONTRACTION: WOLFAGE-SENSITIVE CALCIUM CHANNELS. GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS

BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (14VA) GROUP AND ARE BLOCKED BY OMEGA-AGATILA). THE MAN DEAT GOMEGA-AGATOXIN-1

IIIA (OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-1

IIIA (OMEGA-CONOTOXIN-GVIA) (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-1

CALCIUM CHANNELS CONTAINING ALLPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.

CALCIUM CHANNELS CONTAINING ALLPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.

COMPLEXES, CONSISTING OF ALLPHA-1, ALPHA-1B SUBUNIT SUBUNIT SUBUNIT SUBUNIT SUBUNIT SUBUNIT SUBUNITY SUBCELLULAR LOCATION INTERRAL NERVORES ENERGY AND ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCUE ON ALPHA-1B-2 ARE PRODUCED BY ALTENANILES CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENT (S4): S4 SEGMENTS

-1- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE POOMAIN: EACH OF THE FOUR INTERNAL (REVORMS AND ARE CHARACTERIZED BY SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION

-1- TOWAIN: PROSPHOBLY THE YOUTGE-SENSOR AND ARE CHARACTERIZED BY SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION

-1- THE PROSPADILY REPRESENT THE AUGUNITY SERIES OF POSITI
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams M.E., Brust P.F., Feldman D.H., Patthi S., Simerson S.,
Maroufi A., McCue A.F., Velicelebi G., Ellis S.B., Harpold M.M.;
"Structure and functional expression of an omega-conotoxin-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92335886; PubMed-1321501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human N-type calcium channel.";
Science 257:389-395(1992).
                                                                                                                                                                                                                                                                                                     CACNAIB OR CACNLIAS OR CACHS.
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III) (BIII).
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CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).
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CALCIUM ION SELECTIVITY AND PERMEABILITY
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CALCIUM ION SELECTIVITY AND PERMEABILITY
InterPro; IPR002077; -.
InterPro; IPR002077; -.
Edfan, PF00520; ion_trans; 4.
PRINTS; PR00167; CACHANNEL.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
                                                   Calcium channel; Glycoprotein; Repeat; Multigene family;
Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing
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                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).

S4 OF REPEAT II (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

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S6 OF REPEAT II (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

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                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GSGSVNGSPLLSFGSGASTPORGGRRQLEOTPLTPPRSITYR
TANSSPHFAGAOTSLPAFSFGRLSRGLSEHAALLQRDPLS
QPLAPGSRIGSDPYLGORLDSEASVHALPEDTLFEEAVAT
NSGRSSRTSYVSSLTSQSHPLRRVPNGYHCLGLSSGGRAR
HSYHHDDQDHWC -> AGGANGFPRTTPCCRETPSASSWPL
ALELALITUMGSWYUVRDLSTPCLRFSLSRRWPPTRAAP
PGLPTCPP (IN ISOFORM ALPHA-1B-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :|: || :| || 318 BPGAREERPRPHRSHSKEAAGPPEARSERGRGPGPEGGRRHHRR--GSPEEAAEREPRRH 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 EPSEQED----SSSAERGLGPSPA----GDGPSGSGKHHRQAPGLLWDA----- 48
PHOSPHORYLATION (BY CAPK) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheung A.K.;
Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE WILLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELBULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF PHOSPHORILATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 -SHQQEQPTSSSHHGGAGAV-EIRSRHSSYP-AGTEDDEGMGEEPS-PFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence analysis of the immediate-early gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

DOMAIN 390 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 90; DB 1; Length 2339; 30.8%; Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0cT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 17:4637-4646(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89315207; PubMed=2546124;
                                                                                                                                                                                                                                                                                                                                                                                                             262494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE-EARLY PROTEIN IE180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X15120; CAA33214.1; -. PIR; S04713; EDBEIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
1719
1748
256
1563
1675
2339
                                                                                                                                                                                                                                                                                                                                                                                                         2339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31523;
1719
1737
256
1563
1675
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P11675;
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                                   CA_BIND
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                   CARBOHYD
                                                                                                                                      CARBOHYD
                                                                                                                                                                   VARSPLIC
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chromogranin A.";
FEBS Lett. 404:87-90(1997).
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  8
                                                                                                     13-AUG-1987 (Rel. 05, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I)
[CONTAINS: VASOSTATIN-1; CHROMOSTATIN; CHROMACIN; PANCREASTATIN; WE-14; CATESTATIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86311345; PubMed-3018587;
Iacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.;
"Bovine chromogranin A sequence and distribution of its messenger RNA
in endocrine tissues.";
                                                                                                                                  48 ASHQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEEPSPFRGRSRSAP 101
                                                                                                                                                       291 RSPVSSNPNSSSSSTTTVAVEPVAR-----GPEKDEDGLGLAGDGGAPLQRQPRRRAG 344
                                                                   Gaps
                                                                                        --APGLLWD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primary structure of bovine chromogranin A: a representative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kang Y.K., Yoo S.H.; "Identification of the secretory vesicle membrane binding region of
                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-92140395; PubMed-1779968;
Iacangelo A.L., Grimes M., Eiden L.E.;
"The bovine chromogranin A gene: structural basis for hormone regulation and generation of biologically active peptides.";
Mol. Endocrinol. 5:1651-1660(1991).
                                             Length 1461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
Levine M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86300648; PubMed-3755681;
Beneddun U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell
Mallet J., Huttner W.B.;
"The primary structure of bovine chromogranin A: a represent
                                                                                                                                                                             102 PNLWAAQRYGRELRRMSDEFVDS----FKKGLPRPKSAGTATQMRQSSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a class of acidic secretory proteins common to a variety of peptidergic cells.";
EMBO J. 5:1495-1502(1986).
                                                                                                                                                                                                  345 E---GALRRGRGFSSSSGGSDSDLSPARSPSAPRAPAAAAAARRSASS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary structure of bovine pituitary secretory protein (chromogranin A) deduced from the cDNA sequence."; Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
POLY-SER.
W; 7F31E7ABE403B208 CRC64;
                                                                  Indels
                                                                  70;
                                            DB 1;
                                         Score 89.5; DB; Pred. No. 14; 9; Mismatches
                                                                                      9 PSEQEDSSSAERGLGP -- SPAGDG - PSGS -- - GKHHRQ -
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                                                                                                                                                                                                                                                          449
                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97228583; PubMed=9074643;
          149833 MW;
                                            9.9%;
                                                                  50; Conservative
                                                                                                                                                                                                                                                           STANDARD;
 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 323:82-86(1986).
                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos
         1461 AA;
                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                     P79392;
                                                                                                                                                                                                                                                         CMGA_BOVIN
P05059; P79
                                           Query Match
Best Local Si
Matches 50;
DOMAIN
SEQUENCE
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MEDLINE-97439785; PubMed-9294131; Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H., Gill B.M., Parmer R.J.; "Novel autocrine feedback control of catecholamine release. A discrete chromogranin a fragment is a noncompetitive nicotinic cholinergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3D-STRUCTURE MODELING OF CATESTATIN.
MEDLINE-99025667; PubMed=9809795;
Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
Khan I., Parmer R.J., O'Connor D.T.;
"Mechanism of action of chromogranin A on catecholamine release:
molecular modeling of the catestatin region reveals a beta-
strand/loop/beta-strand structure secured by hydrophobic interactions
and predictive of activity.";
Regul. Pept. 77:43-53(1998).
                                                                             Yoo S.H., Albanesi J.P.; "Ca2(+)-induced conformational change and aggregation of chromogranin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Chromaffin granules;
MEDLINE-97067080; PubMed-8910482;
Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,
van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.,
"Antibacterial activity of glycosylated and phosphorylated
chromogranin A-derived peptide 173-194 from bovine adrenal medullary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89331945; PubMed-2756155;
Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P., Chang D., Tatemoto K.;
"Isolation and characterization of bovine pancreastatin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION OF CATESTATIN.
MEDLINE-99000113; PubMed-9786174;
Kennedy B.P., Mahata S.Y., O'Comor D.T., Zlegler M.G.;
"Mechanism of cardiovascular actions of the chromogranin A fragment
                                                                                                                                                                                                                                                                                                                                                                                                         À
                                                                                                                                                                                                                                                                      SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
MEDLINE-91142185; PubMed=1996343;
Galindo E., Rill A., Bader M.-F., Aunis D.;
"Chromostatin, a 20-amino acid peptide derived from chromogranin inhibits chromaffin cell secretion.";
Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
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MEDLINE=20219105; PubMed=10753865;
Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet
Aunis D., Metz-Boutigue M.H.;
"Antibacterial and antifungal activities of vasostatin-1, the N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [15]
CABOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galindo E., Rill A., Bader M.-F., Aunis D.;
Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
SEQUENCE OF 19-45, AND CALCIUM-BINDING.
MEDLINE=90354431; PubMed=2387861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        terminal fragment of chromogranin A.";
J. Biol. Chem. 275:10745-10753(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromaffin granules.";
J. Biol. Chem. 271:28533-28540(1996).
                                                                                                                                                                                                Biol. Chem. 265:14414-14421(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 191-212 (CHROMACIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION OF CATESTATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regul. Pept. 25:207-213(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides 19:1241-1248(1998).
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                                                                                                                                                                                                  EUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM
CHROMAFFIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-
COMPETITIVE NICOTINIC CHOLINERGIC ANTAGONIST.
FUNCTION: VASOSTATIN-1 HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-
POSITIVE BACTERIA M.LUTEUS, B.MEGATERIUM. NOT ACTIVE AGAINST GRAM-
POSITIVE BACTERIA B.CEREUS, B.SUBTILIS, S.PYROGENES, M.FORTUITUM,
S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-NEGATIVE BACTERIA
E.COLI, E.CLOACAE, S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURUGINOSA.
A.BRASSICOLA, N. HEMATOCOCCA, F. CULMORUM AND F. CXYPORUM AND
AGAINST S.CEREVIASE AND C.ALBICANS YEAST. INACTIVE AGAINST
                                                                                                                                                                       -!- FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
              Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.; "Chromogranin A from bovine adrenal medulla: molecular characterization of glycosylations, phosphorylations, and sequence heterogeneities by mass spectrometry."; hall blochem. 274:69-80(1999).
-1- FUNCTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN
                                                                                                                                     -1- FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                               MASS SPECTROMETRY: MW-8584.9; METHOD-MALDI; RANGE-19-94.
MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Amidation; Glycoprotein; Calcium-binding; Phosphorylation; Polymorphism; 3D-structure; Antibiotic; Fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMOGRANIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANCREASTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASOSTATIN-1.
CHROMOSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATESTATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMACIN
MEDLINE=99459228; PubMed=10527498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, S79270; AAB21297.1; -. EMBL, S79256; AAB21297.1; JOINED. EMBL, S79258; AAB21297.1; JOINED. EMBL, S79260; AAB21297.1; JOINED. EMBL, S79262; AAB21297.1; JOINED. EMBL, S79264; AAB21297.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0659; CHROMOGRANIN.
PROSITE; PSO0422; GRANINS_1; 1.
PROSITE; PSO0423; GRANINS_2; 1.
                                                                                                                     RELEASE FROM THE PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M16971; AAA30765.1; -
EMBL; U7323; AAC48700.1; -
PIR; A41520; A41520.
PIR; A24175; A24175.
PIR; A28033; A28033.
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AAB21297.1;
CAA27636.1;
                                                                                                                                                         FROM CHROMAFFIN CELLS.
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GlycoSuiteDB; P05059; -
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S79268;
X04012;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoprotein gene.".

J. Dent. Res. 76:754-760(1997).

-! FUNCTION: COULD BE INVOLVED IN THE INDUCTION OF MINERALIZATION OF

EXTRACELLULAR MATRIX AND IN DENTINOGENESIS.

-! TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH

PARTICULARIX IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESSED

IN LIVER AND SKIN.
                                                                                                                                                                                                                   63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSD--- 119
                                                                                                         Gaps
                                                                                                                                                                  138 EVEKSDEDSDGDRPQASPGLGPGP-----KVEEDNQAPG-----EEEEAPSNAH-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.; "Cloning and expression analysis of the bovine dentin matrix acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                       6 EFEPSEQE---DSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last annotation update)
DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1 PRECURSOR (DENTIN MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 510;
                                                                           Length 449;
                                                                                                      57; Indels
 PHOSPHORYLATION (PARTIAL).
              PHOSPHORYLATION.
PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION.
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                                                                                                                                                                                                                                                            120 -EFVDSFKKGLPR------PKSAGTATQMRQSSSW 147
                                                                           DB 1;
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No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                    510 AA
                                                                          Score 88.5; D
Pred. No. 5.1;
                                                                                                        19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55491 MW;
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                                                                           9.88;
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Best Local Similarity
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MEDLINE-93041287; PubMed-1419850;
Maler D., Stumm G., Ruhn K., Preiss A.;
Maler D., Stumm G., Ruhn K., Preiss A.;
"Hailess, a Drosophila gene involved in neural development, encodes a novel, serine rich protein.";
Mech. Dev. 38:143-156(1992).
"I- FUNCTION: IS A POTENT ANTAGONIST OF NEUROGENIC GENE ACTIVITY DURING SENSORY ORGAN DEVELOPMENT. THE EXPRESSION OF DISTINCT CELL FATES BY THE TRICHGEN (SHAFT) / TORMOGEN (SOCKET) SISTER CELL FATES BY THE TRICHGEN (SHAFT) / TORMOGEN (SOCKET) LEVEL PAIR DEPENDS ON THE LEVEL OF H ACTIVITY: A CERTAIN THESHOLD LEVEL OF H ACTIVITY: A CERTAIN THESHOLD LEVEL OF H ACTIVITY IS REQUIRED, BELOW WHICH BOTH SISTER CELLS ADOPT THE
                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                              Bang A.G., Posakony J.W.;
"The brosophila gene Hairless encodes a novel basic protein that
controls alternative cell fates in adult sensory organ development.";
Genes Dev. 6:1752-1769(1992).
                                                  347 PSQENSSESQEEALHES-RGDNPDNATSHSRE-----HQADSESSEEDVLDKPSDS 396
                                                                             ----QEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWA 106
                                                                                                   397 ESTSTEEQADSESHE----SLRSSEES-PESTEEQNSSSQEGAQTQSRSQESP---- 444
   Gaps
                           -- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- TISSUE SPECIFICITY: OVARY, EMBRYOS, LARVAL AND PUPAL IMAGINAL
  55;
  Indels
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  51;
                          PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQ-
                                                                                                                              145
                                                                                                                                                     ----SEEDDGSDSQDSSRSKEDSNSTESVSSS 472
                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                             107 AQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQSS
                                                                                                                                                                                                                     PRT; 1077 AA
  Mismatches
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POLY-ALA.
POLY-ALA.
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 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l protein; Nuclear
115 123 TH
                                                                                                                                                                                                                                              Created)
  Conservative
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                                                                                                                                                                                                                     STANDARD;
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891
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(Rel. 28,
(Rel. 28,
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37;
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Nature 366:170-174(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                   73 HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khavari P.A., Peterson C.L., Tamkun J.W., Mendel D.B., Crabtree G.R.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                           678 SSSSSG---KKCGDHPAAIISNVHHPQ-----HSMYQPSSSSYPRAL---LTSP 721
                                                                                                                                                                                                                                                                                                                            15 SSSAERGLGPSPAGDGPSG--SGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chiba H., Muramatsu M., Nomoto A., Kato H.;
"Two human homologues of Saccharomyces cerevisiae SWIZ/SNF2 and
Drosophila brahma are transcriptional coactivators cooperating with
the estrogen receptor and the retinoic acid receptor.";
Nucleic Acids Res. 22:1815-1820(1994).
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Brower A., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu :
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: TRANSCRIPTIONAL COACTIVATOR COOPERATING WITH NUCLEAR HORMONE RECEPTORS TO POTENTIATE TRANSCRIPTIONAL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
1-OCT-2000 (Rel. 40, Last annotation update)
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1
PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       DB 1; Length 1077;
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  S -> A (IN REF. 2).
OH -> LL (IN REF. 2).
A -> R (IN REF. 2).
AAVA -> RLLP (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                      A94BF1A27579E2F1 CRC64;
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-> A (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1647 AA.
                                                                                                                                                                                                                    9.6%; Score 86.5; D
28.9%; Pred. No. 18;
ive 17; Mismatches
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SMARCA4 OR SNF2L4 OR BRG1 OR SNF2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94268902; PubMed=8208605;
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MEDLINE-94050144; PubMed-8232556;
                                                                                                                                         111039 MW;
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P51532;
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                                                 the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                  9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH---RQAP-GLLWDASHQQEQPTSSSHHGGA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                30 PSPGPSPGSAHSMAGPSP---GPPSAG--HPIPTQGPGGYPQDNMHQMHKPMESMHEKGM 84
                                                                                                                                                                                          Pfam; PF00176; SNF2_N; 1.

Pfam; PF00439; bromodomain; 1.

Pfam; PF00513; helicase_C; 1.

PRINTS; PR00503; BROMODOMAIN.

PROSITE; PS00643; BROMODOMAIN. 1; 1.

PROSITE; PS50014; BROMODOMAIN. 2; 1.

Transcription regulation; Nuclear protein; Activator; Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr. Tani M., Lazzarini R.A.;

"Expression of a homeo domain protein in noncontact-inhibited cultured cells and postmitotic neurons.";

Genes Dev. 1:482-496(1987).
                                                                                                                                                                                                                                                                                                                                                                                         Length 1647;
-!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                               POLY-GLU.
IW; 7B785E7953277F1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQ 108
                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HOMEOBOX PROTEIN HOX-A5 (HOX-1.3) (M2).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                POLY-LYS.
POLY-GLU.
ATP (POTENTIAL).
DEGH BOX.
                                                                                                                                                                                                                                                                                                                                                                                         Score 86.5; DB Pred. No. 27; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 AA
                                                                                                                                                                                                                                                                                                                           POLY-GLU.
BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE=88056292; Pubmed=2890554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2],
SEQÜENCE FROM N.A.
MEDLINE-88328807; Pubmed=2901335;
                                                                                                                EMBL; U29175; AAB40977.1; -. EMBL; D26156; BAA05143.1; -. EMBL; AC006127; AAC97987.1; -. MIM; 603254; -.
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 29.8%;
Matches 31; Conservative 9
                                                                                                                                                                                                                                                                                                                                                          184585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                           Interpro; IPR000330; -.
Interpro; IPR001487; -.
Interpro; IPR001650; -.
                                                                                                                                                                                                                                                                                                                                    1547
                                                                                                                                                                                                                                                                        Helicase.
                                                                                                                                                                                                                                                                                                                        1360 136
1477 154
1571 158
1647 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HXA5_MOUSE
P09021;
                                                                                                                                                                                                                                                                                                     NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 15:1313-1322(1996).

-1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS. ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF: 5'-CYNATTA[TG]Y-3'.

-1- SUBCELLUIAR LOCATION: NUCLEAR.

-1- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 YSQPATSTHSPPPDPLPCSAVAPSPGSDSHHGGKNSLGNSSGASANAGSTHISSREGVGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 SEQ-EDSSSAERG------LGPSPAGDGPSGSGKHHRQ-----APGLLWDASHQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 QEQPTSS-----AGAVEIRSR----
                                                                                                                                                                                                                                                                                                      'The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
                                                        "Coding sequence and expression of the homeobox gene Hox 1.3."; Development 102:349-359(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00025; ANTENNAPEDIA.
PROSITE; PS000027; HOMEOBOX_1: 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS50071; HOMEOBOX_2: 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                   MEDLINE-89232713; PubMed-2565857;
Odenwald W.F., Garbern J., Arnheiter H., Tournier-Lasserve E.,
Kessel M., Colberg-Poley A.M., Labeit S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86; DB 1; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DC4BDDA8FE62766E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE=96205869; PubMed=8635464;
Zhao J.J., Lazzarini R.A., Pick L.;
"Functional dissection of the mouse Hox-a5 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.5%; Score v.,
25.8%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M36604; AAA37838.1; -.
EMBL; Y00208 CAA68364.1; -.
EMBL; X16640; CAA633478.1; -.
EMBL; M28021; AAA37837.1; -.
PIR; SO7812; MJMS13.
HSSP; P02833; 1SAN.
TRANSPAC; T00377; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:96177; Hoxa5.
InterPro; IPR001356; -.
InterPro; IPR001827; -.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                          Genes Dev. 3:158-172(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation.
DOMAIN 176 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 25.89 les 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 AA;
                               Lehrach H., Gruss
                                                                                                                                                                                                                                                                      Lazzarini R.A.;
                                                                                                                                                                                                                                                                                                                                          phosphoprotein
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us-09-580-523-1.rsp

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ACT_SITE
SEQUENCE
    BINDING
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146 ASAAEEDAPASSE-QAGAQSEPSP-----APPAQPQIYPWMRKLHISHDNI-----G 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTIVATES THE JNK PATHWAY. IMPLICATED IN THE REORGANIZATION OF THE ACTIN CYTOSKELETON AND IN THE FORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN PROSTATE, TESTIS, AND
                                                                                                                                                                                                                                                             01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE PAK 4 (EC 2.7.1.-) (P21-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLON.
-1- PIM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ^{n}PAK4, a novel effector for Cdc42Hs, is implicated in the reorganization of the actin cytoskeleton and in the formation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND WEAKLY WITH RAC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
PubMed=9822598;
Abo A., Qu J., Cammarano M.S., Dan C., Fritsch A., Baud V.,
Belisle B., Minden A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKER.
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50108; GBD; 1.
PROSITE; PS00107; PROTEIL_KINASE_ATF; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
                                                                                                                                                                                               591 AA
                                                                      GPEGKRARTAYTRYQTLELEKEFH--FNRYLTR 222
                                           129 LPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 GBD DOMAIN.
                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 17:6527-6540(1998).
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                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00518; 1PHK.
InterPro; IPR000095; -.
InterPro; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
320
572
335
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                               KINASE 4) (PAK-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melnick M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 605451;
                                                                                                                                                                      PAK4_HUMAN
ID PAK4_HUMAN
AC 096013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      filopodia
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NP_BIND
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                                                                                    192
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 151-160; 235-244 AND 267-282, AND PHOSPHORYLATION SITES. MEDLINE-94237860; PubMed-8182057; Butt E., Abel R., Krieger M., Palm D., Hoppe V., Hoppe J., Walter U.; "CAMP- and cGMP-dependent protein kinase phosphorylation sites of the focal adhesion vasodilator-stimulated phosphoprotein (VASP) in vitro
                                                                                                                                                                                                                                                                                                                                      64 AGAVEIRSR---HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning, structural analysis and functional expression of
the proline-rich focal adhesion and microfilament-associated protein
VASP.";
                                                                                                                                                                                                                                                                                                    63
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-I- FUNCTION: ACTIN AND PROFILIN-BINDING MICROFILAMENT-ASSOCIATED PROPEIN. MAY ACTIN CONCERT WITH PROFILIN TO CONVEY SIGNAL TRANSDUCTION TO ACTIN FILAMENT PRODUCTION.
                                                                                                                                                                                                                                                                                                4 IPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zimmer M., Fink T., Fischer L., Hauser W., Scherer K., Lichter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haffner C., Jarchau T., Reinhard M., Hoppe J., Lohmann S.M.,
                                                                                                                                                                 DB 1; Length 591;
10;
                                                                                                                                                   04C2A5C0B06427D5 CRC64;
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
VASP_HUMAN STANDARD; PRT; 380 AA.
AC P50552, 093035;
DT 01-0CT-1996 (Rel. 34, Last sequence update)
DT 01-0CT-1996 (Rel. 34, Last sequence update)
DT 01-0CT-2000 (Rel. 40, Last annotation update)
DT 01-0CT-2010 (Rel. 40, Last annotation update)
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-!- SUBCELLULAR LOCATION: FOCAL ADHESIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-95129547; PubMed-7828592;
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J. Biol. Chem. 269:14509-14517(1994).
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MEDLINE=96411679; PubMed=8812448;
                                                                 64071 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 DV----GTPQP--AGLAS 195
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                                                                 591 AA;
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Peretz H.;
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                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.ch).
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
PTM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT PROTEIN KINASE (CGPK) IN PLATELETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 AAAHGAGGGPPPAPPLPAAQGPGGGG---AGAPGLAAAIAGAKLRKVSKQEEASGGPTAP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 KAESGRSGGGLMEEMNAMLARRKATQVGEKTPKDESANQEEPEARVPAQSESVRRPWE 311
                                                                                                                                                                                                                                                                                                                                                                                                               60; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SAERGLG-----PSPAGDGPSGSGKHHRQAPGL-----LWDASHQQEQ---PTS- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res., 5:31-39(1998).
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POLY-GLY.
POLY-GLY.
POLY-GLY.
POLY-SER.
PHOSPHORYLATION (BY CAPK AND CGPK).
PHOSPHORYLATION (BY CAPK AND CGPK).
PHOSPHORYLATION (BY CAPK AND CGPK).
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Thornton M.A., Poncz M., Korostishevsky M., Yakobson E., Usher S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.4%; Score 85; DB 1; Length 380; Best Local Similarity 24.9%; Pred. No. 7.8; Matches 43; Conservative 18; Mismatches 52; Indels
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01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
HYPOTHETICAL PROTEIN KIAA0553.
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Phosphorylation; Actin-binding.
122 POLY-PRO.
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                                                                                                                                                              X98534; CAA67147.2; -. X98533; CAA67147.2; JOINED.
                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                 EMBL; Z46389; CAA86523.1; -.
                                                                                                                                                                                                                                                                                                                                               39830
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                                                                                                                                                                                                  InterPro; IPR001960;
Pfam; PF00568; WH1; 1
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NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 SYSDYSDRSRRHSKRSHDSDDSDYASSKHRSKRHKYSSSDDDYSLSCSQSRSRSHTRE 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 PSQYSEEEEEEDSGSEHSRSRSGRRHSSHRSSRRSYSSSSDASSDOSCYSRQRSYSDD
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"The human platelet alphaIIb gene is not closely linked to its integrin partner beta3."; Blood 94:2039-2047(1999).
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POLY-GLY.
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Best Local Similarity 19.9%; Pred. No. 23;
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EMBL; AF160252; AAF03681.1; -.
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263 26
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Q90889 homo sapien
Q98321 molluscum c
Q9epu2 rattus norv
Q90000 mus musculu
Q9ne12 caenorhabdi
                                                                                                            Ognxig homo sapien
Oghau3 homo sapien
O15206 homo sapien
O05331 homo sapien
O99w76 drosophila
O91wj9 oryza sativ
Q91ff8 arabidopsis
                                                                                                                                                                                                                                                                                   O9jig4 mus musculu
O08719 rattus norv
P70429 mus musculu
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Q9eru8 mus musculu
097643 lama glama
              025734 plasmodium
036421 alcelaphine
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Oghbb5 homo sapien
O97645 macropus ru
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ottilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,
Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;
Elol. Chem. 0:0-0(1997).
EMBL; AF021792; AAB72092.1;
EMBL; AF031523; AAB88124.1; -.
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MEDLINE=97083574; PubMed=8929532;
MARDINE=97. Rapp U.R., Reed J.C.;
"BG1-2 targets the protein kinase Raf-1 to mitochondria.";
Cell 87:629-638(1996).
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SEQUENCE FROM N.A.
Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequen
01-NOV-1998 (TrEMBLrel. 08, Last annotati
BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT)
                                                                                                              Q9NXI9
Q9HAU3
Q15206
Q05331
Q9VW76
Q9LWJ9
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Q9HBB5
O97645
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PRELIMINARY;
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Best Local Similarity
Matches 168; Conserv
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070256 rattus norv
09jhx1 rattus norv
0919n2 brachydanio
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1 MFQIPEFEPSEQEDSSSAER.....RVFQSWWDRNLGRGSSAPSQ
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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035147
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0919N2
0905K9
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0908D2
09FVZ6
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09FVZ6
095N26
095N26
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Gapop 10.0 , Gapext 0.5
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Q9H0B9
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate:*
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7: sp_mhc:*
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sp_vertebrate:*
sp_virus:*
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sp_phage:*
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Q919N2 PRELIMINARY; PRT; Q919N2; 01-0CT-2000 (TrEMBLrel, 15, Created)
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Hsu S.T., Hsueh A.J.W.;

"Interference of BAD (Bcl.xL/Bcl.2-associated death promoter)-induced apoptosis in mammallan cells by 14-3-3 isoforms and Pll.";

Mol. Endocrinol. 11:1858-1867(1997).

EMBL; AF003523; AAC33374,1;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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10.AUG-1998 (TrEMBLrel. 07, Last sequence update)
01.-CCT-2000 (TrEMBLrel. 15, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D'Agata V., Magro G., Travali S., Musco S., Cavallaro S., "Oloning and expression of the programmed cell death regulator Bad the rat brain.";
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70.3%; Score 636.5; DB 11; Length 205;
Best Local Similarity 75.1%; Pred. No. 3.1e-51;
Matches 127; Conservative 11; Mismatches 24; Indels 7;
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22468 MW; 04DD3EBA03B11168 CRC64;
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Last annotation update)
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MEDLINE=98034386; PubMed=9369453;
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                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                   PRELIMINARY;
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Rattus norvegicus (Rat).
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60 HHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSD 119
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Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;

"Functional characterization of two splice variants of rat bad and
their interaction with bcl-w in sympathetic neurons.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF279911; AAF91428.1; --
SEQUENCE 220 AA; 24278 MW; E27BCCD7C969E90F CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D. "Functional characterization of two splice variants of rat bad and their interaction with bel-w in sympathetic neurons.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR031227; AAC15100.1;
EMBL, AR279910; AAF914271: -
SEQUENCE 205 AA: 22228 MW; 7AFA71DAE9CF4A81 CRC64;
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Last annotation update)
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391 EKEKSFMADNGMGPSRGGGKPFGRGGRGRRGPTLASGTNSEASNASE--TESDH----- 442
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                                                                                                                                                                                                                                    MEDLINE-20501263; PubMed-11046149;
Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;
Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;
"Characterization of dFML, a Drosophila melanogaster Homolog of the Fragile X Mental Retardation Protein.";
Mol. Cell. Biol. 20:8536-8547(2000).
EMBL; AR305882; AAG22046.1; - SEGA0689F7EDFBS CRC64;
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Lu R., Misra V.;
"Zhangfei: a second cellular protein interacts with herpes simplex virus accessory factor HGF in a manner similar to Luman and VP16.";
Nucleic Acids Res. 28:246-2454(2000).
EMBL; AF039942; AAD28325.1;
InterPro; IPR001871;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2011 (TrEMBLrel. 16, Last sequence update)
01-MAR-2011 (TrEMBLrel. 16, Last annotation update)
01-MAR-2011 (TrEMBLrel. 16, Last annotation update)
RE DOMAIN CONTAINING RNA-BINDING PROTEIN FMRI.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostarlophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 98; DB 4; Length 272; 28.2%; Pred. No. 0.15; ive 13; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
SEQUENCE 272 AA; 28859 MW; B1F94B438F0702BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.
                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 98.5; DB 13; 32.3%; Pred. No. 0.29; ive 8; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 VEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 --- RDELSDWSLAPTDEESMGYPKRAPDGRKRGGGP 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20330366; PubMed=10871379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 GLPRPKSAGTATQMRQSSSWTR 149
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.9
Best Local Similarity 32.3
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09NS37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09NS37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BABOON LYMPHOCRYPTOVIRUS BA65;
Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
Hayward G.S.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF200364; AAF23950_1; -.
EMBL; AF200364; AAF23950_1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 DEGMGEEP----SPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                MEDLINE-20373792; PubMed-10917738;
Inohara N., Nunez G.;
"Genes with Homology to Mammalian Apoptosis Regulators Identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 ETGVAEDPHMLGDPFRPRSRSAPPALWAAKKYGQQLRRMSDE----FDXGMKRVKSAGTA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG----GA 64
                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Crantata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.9%; Score 207.5; DB 13; Length 95; 50.0%; Pred. No. 4.3e-12; ive 10; Mismatches 24; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ORPSGPTGGHPAAPGAPGPPNPERGSGPADPP---AATRLPLEPR 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100; DB 14; Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                   95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
01-OCT-2000 (TrEMBLral. 15, Last sequence update) 01-MAR-2001 (TrEMBLral. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 TQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 ROMSQSPSWLAFL---WSHKESDAESRPAE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%;
ilarity 33.3%;
Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY)
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10394;
                                              BAD (FRAGMENT).
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01-MAY-2000 (
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Q9DF20;
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Q9Q5K9;
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Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V., Ouackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (CGT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC078840; AAG136311; - SEQUENCE 867 AA; 94083 MW; 4FEA69EIBFCOCB2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 PSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ::| || || || :| || 330 KEEAAAARGGGGDDPLSHSHLGGGGGTGKEAAAAPTPTRGASRGGGGADADAGSEQEDAA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790 AWGGGPDPLSHSHLGGGG------GTGKEEA-AAAPTPTRGASRGGGGGTGT 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 ESDEKASKSEHESEVKEGSDGRAEEASPAPS-PAGESDEKASKSEHESEVKEGSDGRAEE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 -----QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ESEAKEGSDGRAEEASPAPSPAGESDEKASKSEHESEVKEGSDGRAEEASPAPS---PAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 EDSSSAERGLGPSPAG----DGPSGSGKHHRQAP-------GLLWDASHQQE--- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- DGPSGSGKHHRQAPGLLWDAS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 HQQEQPTSSSH-----HGGAGAVEIRSRHSSYPAGTEDD----------EGMGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen & Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D., Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN 2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 10.7%; Score 97; DB 5; Length 1146; Best Local Similarity 23.2%; Pred. No. 0.82; Matches 46; Conservative 18; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1146 AA; 126154 MW; 89FC26E433768B8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-077-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                       Query Match 10.8%; Score 97.5; DB Best Local Similarity 28.0%; Pred. No. 0.55; Matches 37; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00648; Peptidase_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSSIBLE CALPAIN-LIKE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 EFEPSEQEDSSSAERGLGPSPAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00704; CALPAIN. SMART; SM00230; CysPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                       SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 QRYGRELRRMSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| | | :
836 RREERRLGRREE 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                          NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-TREU927;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A. Set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL136118; CAB66246.1; -.
InterPro; IPR00448; -.
InterPro; IPR005383; -.
Pfam; PR005383; HHH; 1.
SMART; SM00278; HHH; 1.
SMART; SM00278; HHH; 1.
SEQUENCE 355 AA; 36853 MW; EIE9D0A574CCABDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 -HSSYPAGTEDDEGMGEEPSPFRGRSRSAP--PNLWAAQRYGRELRRMSDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 SSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG--GAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TASATSGPGRAPASDGRLA----HRRAPGSRTHARHR----SHARHGRRHAAPEELRRR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 355; 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown S.P., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE REPLICATION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     867 A.A.
                                                                                                                                           355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 10.8%; Score 98; DB Local Similarity 28.5%; Pred. No. 0.2; es 43; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 PRPKSAGTATQMRQSSSWTRVFQSWWDRNLG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 DAPTGPGTAWRERAGSALRERMPLWLQTRCG 136
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=43(2);
MEDLINE=97000351; PubMed=8843436;
194 GLARLLSRLSGVGLRLTTSLFR 215
                                                                                                                                                                                                                                                            PUTATIVE DNA-BINDING PROTEIN.
                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
                                                                                                                                                                                                                                                                                  SCC123.06C
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Best Loca Matches

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RESULT 10

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Gaps

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2442 HASSGATGRSPRTPRASGPACASPSRHG---RRLPNGYYPA--HGLARPRGPGSRKGLHE 2496
                                                                       MEDLINE-20219126; PubMed-10753886;
Toru S., Murakoshi T., Ishikawa K., Saegusa H., Fujigasaki H.,
UChihara T., Nagayama S., Osanai M., Mizusawa H., Tanabe T.;
"Spinocerebellar ataxia type 6 mutation alters P-type calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2335 TSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPGPARSESPRACRHGGARWPASG 2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GRS----RSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 SSSAERGLGPSP---AGDGPSGSGKHHRQAP---------GLLWDAS- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 -HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEE-----PSPFR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L5204.2.
L5204.2.
Leishmania major.
Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 SEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M., Cawthra J., Marsolini F., Sunkin S., Stuart K.D.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          69
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 2506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Indels
                                                                                                                                                                                                                                                                                                                                                D64A6C75284A1B53 CRC64;
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SEQUENCE 923 AA; 103964 MW; C229C15F6448F7C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.6%; Score 95.5; DB 5; 1 Similarity 26.4%; Pred. No. 0.9; 33; Conservative 21; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 96.5; E; Pred. No. 2; 18; Mismatches
                                                                                                                                              function.";
J. Biol. Chem. 275:10893-10898(2000).
EMBL; AB035727; BAA94766.2; -.
InterPro; IPR000636; -.
InterPro; IPR000637; -.
InterPro; IPR001682; -.
                                                                                                                                                                                                                                                                                                                                                282580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, CTEMBLrel. 15, ITEMBLrel. 16, I
                                                                                                                                                                                                                                                                                                                                                                                                   10.7%;
25.1%;
                                                                                                                                                                                                                                                                                      Pfam; PF00520; ion_trans; 4
PRINTS; PR00167; CACHANNEL.
SMART; SM00384; AT_hook; 1.
SEQUENCE 2506 AA; 282580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC005941; AAF34290.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                        InterPro; IPR002077; -. InterPro; IPR002111; -.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 46; Conserv
                                     SEQUENCE FROM N.A. TISSUE=CEREBELLUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
   NCBI_TaxID=9606;
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01-OCT-2000 (
01-MAR-2001 (
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                                                                                                                                                                                                                                                                         InterPro;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GRS----RSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GTTMDAS- 49
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Black J.L., Snutch T.P., Lennon V.A.;
Partial sequence of Homo sapiens P/Q-type voltage-gated calcium channel alpha 1 [alpha 1A] subunit isolated from small cell lung, carcinoma cell line, SCC 9, cDNA library.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEE-----PSPFR
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 96.5; DB 4; Length 980;
; Pred. No. 0.78;
18; Mismatches 50; Indels 6
                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
VOLTAGE-DEPENDENT P/O TYPE CALCIUM CHANNEL ALPHA LA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF627D9F8BE16D43 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSAERGLGPSP---AGDGPSGSGKHHRQAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPHAIA-VOLTAGE-DEPENDENT CALCIUM CHANNEL.
CACNAIA.
                                                                                                                                                                                  980 AA.
                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              980 AA; 110251 MW;
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Best Local Similarity 25.1%;
Matches 46; Conservative 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00520; ion_trans; 1.
PRINTS; PR00167; CACHANNEL.
                                                                             150 VFQSWWDRNLGRGSSAPS 167
                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                        (FRAGMENT).
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802 AEQRRINIDDR----SPSAGGPASADVEHRSA-----SQPQQPHS---HAGGSAI-V 845
                               70 RSR----HSSYPAGTEDDE-GMGEEPSP----FRGRSRSAPP----NLWAAQRY--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRELRRMSDEFVDSFKK-----GLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 EDSSSAERGLGPSP---AGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI 69
                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 67.3 KDA PROTEIN (FRAGMENT).
DKFZP434B239.
Endergota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL137336; CAB70699.1; -.
Hypothetical protein.
NON_TER 1
SEQUENCE 622 AA; 67337 MW; 11D6CDF0E2D06082 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.5%; Score 95; DB 4; Length 622; Best Local Similarity 27.6%; Pred. No. 0.67; Matches 50; Conservative 17; Mismatches 50; Indels
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                            128 GLPRP 132
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897 GPPQP 901
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Q9NTE2
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Search completed: October 9, 2001, 15:54:56 Job time: 191 sec

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Bad gene mediating apoptosis – used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Bcl-xL/Bcl-2
Human cell prolife
Human BAD mutant a
Human Bad protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shorter murine BAD
bcl-x(L)/bcl-2 ass
Murine BCL-XL/BCL-
Murine BAD protein
                                                                                                                                                       ; Search time 44.37 Seconds
(without alignments)
229.543 Million cell updates/sec
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Mutant BCL-XL/BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MFQIPEFEPSEQEDSSSAER.....RVFQSWWDRNLGRGSSAPSQ 168
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(SIDSB/gcgdata/geneseq/geneseqp/AA1987 DAT:*
(SIDSB/gcgdata/geneseq/geneseqp/AA1987 DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS8/gcgdata/geneseq/geneseqp/AA1982
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                 412676 seqs, 60623988 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                            - protein search, using sw model
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AAB70369
AAW61317
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AAW00385
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AAB126420
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AAG45046
AAR71006
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AAW37878
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N-PSDB; AAV25877.
Homo sapiens.
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Example 8; Fig 1; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 hggagaveirsrhssypagteddegmgeepspfrgrsrsappnlwaagrygrelrrmsde 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral scleosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as cancers, e.g. symphoma and hormone dependent tumours, autoimmune diseases, e.g. systemic lupus erythematosus and immune-mediated aplomerulomephritis and viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad can also be used for
                                             The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-Xl results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH
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ilarity 100.0%; Pred. No. 6.4e-88;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB13512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB13512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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The present sequence is the human APOP-1 protein. This protein, which shares structural and chemical homology with Bcl-2, is involved in cell proliferation. Its coding sequence was isolated by screening a synovial tissue cDNA library using a computer search for amino acid sequence alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated inflammation such as Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus, emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lupus erythematosus, multiphe sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, rheumatoid arvitis, syndrome and autoimmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulation, infections trauma, disorders with associated apoptosis including AIDS and other frauma, disorders with associated apoptosis including AIDS and other curemer and generatic immunodeficiencies, meurodegenerative diseases can canchal infarction, and wasting diseases including cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 hggagaveirsrhssypagteddegmgeepspfrgrsrsappnlwaagrygrelrrmsde 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 905; DB 21;
100.0%; Pred. No. 6.4e-88;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB70368 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APOP-) APOPTOSIS TECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 168; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200110888-A1
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for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      death, reperfusion cell death, wound healing, cancer, viral infections, imporpolative conditions, arthrilis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically claimed human BAD mutant amino acid sequence from the present invention.
                                                                                                                                                                                                                      The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Serlis of a murine BAD (longer murine BAD) or Serlis of a murine BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, notariarchardic, antiischaemic, vulnerary, cytostatic, antiivral, antiarthritic, antiinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polymouleotides can be used for screening candidate compounds and drugs for activities that are accompanied to the compounds and drugs for activities that are accompounds and drugs for activities.
                                               New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                            Claim 1; Page 147; 157pp; English.
WPI; 2001-138734/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Bad protein.
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                                                                                                                         Ser113
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                                                                                                                                         HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                           Gaps
                                                                      1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                     ;
0
     Length 168;
                                                                                                                                                                                                                                121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                       Indels
100.0%; Score 905; DB 22;
100.0%; Pred. No. 6.4e-88;
ive 0; Mismatches 0;
                                    Matches 168; Conservative
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RESULT

AAW32476

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S-phase kinase associated protein; SKP1; SKP2; SKP2-11ke protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic.
AAB48287 standard; protein; 168 AA
                                                                                                                                                                               05-JUN-2000; 2000WO-US15449
                                                                                                                                                                                                  99US-0137494
                                     02-APR-2001 (first entry)
                                                                                                                                       WO200075184-A1
                                                                                                                     Homo sapiens
                                                                                                                                                                                                  04-JUN-1999;
                                                                                                                                                           14-DEC-2000.
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                                                                                                                                                                                                       The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKPL, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin, CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitroring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                    Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 905; DB 22;
100.0%; Pred. No. 6.4e-88;
iive 0; Mismatches 0;
                                                                                                                                                                         Claim 5; Page 102-103; 162pp; English.
                Kondo T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 168; Conservative
                Tsvetkov LM,
                                                WPI; 2001-061703/07.
                                                                                                                                                                                                                                                                                                                                                                                           168 AA;
                                                                                                                                                                                                                                                                                                                                                        treating tumours.
                                                                  N-PSDB; AAC84599
              Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bc1-2
                                                                     BBC6 gene; cell death; cell cycle; Bcl2; human.
                                                     BBC6 protein for regulating cell death.
AAW32476 standard; Protein; 166 AA
                                                                                                                                                             96US-0665617.
                                   (first entry)
                                                                                                                                                                              (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                 WPI; 1997-447980/41.
                                                                                                                                                                                                                           N-PSDB; AAT91561.
                                                                                        Homo sapiens.
                                                                                                                                            18-JUN-1996;
                                                                                                                                                            18-JUN-1996;
                                   15-JAN-1998
                                                                                                        US5663316-A.
                                                                                                                           02-SEP-1997
                                                                                                                                                                                                Xudong Y;
                 AAW32476;
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31-OCT-1995;
                                                                                                                                                                                                                             invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                             The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with BC1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and the rabea antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                         54 QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
                                                                                                                                                                                                                                                                                               52 qptssshhggagaveirsrhssypagteddegmgeepspfrgararpppnlwaagrygre 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                           1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPG-----LLWDASHQQE 53
                                                                                                                                                                                                                                       114 LRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                   16;
                                                                                                                                                                          Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                  6
                                                                                                                                                                          Score 751; DB 18;
Pred. No. 1.2e-71;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 148-149; 157pp; English
           Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Ā
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                                                                                                                                                                                                                                                                                                                                                                                                      AAB70370 standard; protein; 162
                                                                                                                                                                          Query Match 83.0%;
Best Local Similarity 84.0%;
Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                         166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for s
apoptosis, c
Serll3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                              AAB70370;
                                                                                                                                         Sequence
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The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amino acid sequence of a mutant Bel-XL/Bel-2 associated cell death requiator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Serl18 of a human BAD, Serl55 of a murine BAD (longer murine BAD) or Serl13 of a murine BAD, solotropic, antischaemic, vulnerary, cytostatic, antiviral, nootropic, antischaemic, vulnerary, cytostatic, antiviral, antiarthritic, antilnflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include indentified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically contained shorter murine BAD mutant amino acid sequence from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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191..192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.7%; Score 649; DB 22; 75.6%; Pred. No. 6.7e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
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Best Local Similarity
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat corprevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, ciffammation and autoimmune disease. Polynuclectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aping or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family serituted cannot bind 14-3-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQOEQPTSSSH 60
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                                                                                                                                                                                                     New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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96US-0733505
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                                             (UNIW ) UNIV WASHINGTON
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                                                                                                                                                            N-PSDB; AAV27833
18-OCT-1996;
                                                                                             Korsmeyer SJ;
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                                                                                                                                                                                                                                                                                                                                                               This sequence represents the murine bcl-x(L)/bcl-2 associated death correcter (Bad) gene. Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2 related family clustered in the BH1 and BH2 domain. Bad assays and in vivo in mammanian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L) and bcl-2 in yeast two-hybrid death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an II-3 dependent cell line expressing bcl-x(L), and its also counters the countering the death of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-z(L) to form heterodimers. Such agents may be used to treat the prodegenerative diseases, immunodeficiency diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                               Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.7%; Score 649; DB 17; Length 204; 75.6%; Pred. No. 9.1e-61; ive 12; Mismatches 23; Indels 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine BCL-XL/BCL-2 associated cell death regulator.
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                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 1; 130pp; English.
                     94US-0333565.
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N-PSDB; AAT29479.
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                   31-OCT-1994;
                                                                                                              Korsmeyer SJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel serine-phosphorylated protein, BAD (BAL-12 associated cell death regularch. The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator. Addulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphates, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  result from immunodeficiency diseases, senescence, neurodegenerative disease, ischaemic cell death, reperfusion cell death, infertility and wound-healing. Decreased apoptosis may result from cancer, viral infection, lymphoproliferative conditions, arthritis, infertility, infilammation and autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
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cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 649; DB 19; 75.6%; Pred. No. 9.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 8; 61pp; English.
                                                                                                                                                                                                                     97WO-US15871.
                                                                                                                                                                                                                                                                96US-0707868.
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Best Local Similarity 75.69
Matches 127; Conservative
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                                                                                                                    WO9809643-A1.
                                                                                                                                                                                                                                                                                                                                                                 Korsmeyer SJ;
                                                                                                                                                                                                                     09-SEP-1997;
                                                                                                                                                                                                                                                                     09-SEP-1996;
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The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

(I) associated cell death regulator polypeptide (BAD) or its

(I) for acid substitutions at Ser118 of a human

(I) has immunostimulant, neuroprotective,

(I) has immunostimulant, neuroprotective,

(I) notropic, antiinflammatory and immunosuppressive activities, and

(I) antiarthritic, antiinflammatory and immunosuppressive activities, and

(I) antiarthriting apoptosis in a cell. Candidate compounds

(I) immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

(I) death, reperfusion cell death, wound healing, cancer, viral infections,

(I) immunodiferative conditions, arthritis, infertility, inflammation and

(I) autoimmune diseases. The present sequence represents a specifically
immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; Imphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW61317 standard; Protein; 204
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                                                                                                                                                                            musculus
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                                                                                                                                                                                                                    Synthetic.
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us-09-580-523-1.rag

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AAW61316 standard; Protein; 204

12

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AAW61316

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

Mutant BCL-XL/BCL-2 associated cell death regulator #1.

(first entry)

07-0CT-1998

AAW61316;

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control of the treatment of the control of the than Ser at present interaction desiring the control of the than Ser at present in an analysis of the control of the control
                                                                                                                                                                                                                                                                                                                            Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                             Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 60; 95pp; English.
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                                                                                                                 (first entry)
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                                                                                                                 07-0CT-1998
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AAW61317;
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New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection

96us-0733505. 97WO-US19175.

17-OCT-1997; 18-OCT-1996;

WO9817682-A1

Mus sp. Synthetic.

30-APR-1998.

UNIW ) UNIV WASHINGTON

WPI; 1998-261422/23.

Korsmeyer SJ;

N-PSDB; AAV27834

Claim 7; Page 59; 95pp; English.

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologus polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, untant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease, Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, adjug or ischemmic cell death. The apoptotic status of cells is the content of the protein and non-content and n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14.3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14.3-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 AA;
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75.0%; Pred. No. 1.9e-60;
iive 13; Mismatches 23;
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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQOEQPTSSSH 60

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121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

61 86

Best Local Similarity 75.03 Matches 126; Conservative

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**Duery Match** 

us-09-580-523-1.rag

204 AA;

Sequence

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death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, contained and autoinfamune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful.

In treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family Set: substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
                                                                                HCGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRCRSRSAPPNLWAAQRYGRELRRMSDE 120
                    4
New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or
                                                                                                                                    121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                               Mutant BCL-XL/BCL-2 associated cell death regulator #3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 60-61; 95pp; English.
                                                                                                                                                                                                                                                                               AAW61318 standard; Protein; 204 AA.
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                                                                                                                                                                                                                                                                                                                                                           07-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-261422/23.
N-PSDB; AAV27836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korsmeyer SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-0CT-1997;
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 115 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infammation and autoimmune-disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is
                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
                                                                                                                                          61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                              Gaps
                                                                                       1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine substituted mutant; apoptosis; cancer; viral infection.
 Length 204;
                                  Indels
                                                                                                                                                                                                              121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                  Mutant BCL-XL/BCL-2 associated cell death regulator #4.
                                    23;
; Score 643; DB 19;
; Pred. No. 3.9e-60;
14; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                      AAW61319 standard; Protein; 59
71.08;
74.48;
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                                  Matches 125; Conservative
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                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV27837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korsmeyer SJ;
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Synthetic.
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 Query Match
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AAW61319
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phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
  measuring relative amounts of phosphorylated and non-
                                                                                                                                                                                                     59 AA;
  determined by
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888888888888
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ö Gaps 63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEF 121 59 .. O Length 59; Indels Query Match 34.7%; Score 314; DB 19; Best Local Similarity 100.0%; Pred. No. 4.5e-26; Matches 59; Conservative 0; Mismatches 0; ò g

15 AAW61320 RESULT

Ą AAW61320 standard; Protein; 59

Search completed: October 9, 2001, 15:53:27

203 sec

Job time:

AAW61320;

07-OCT-1998 (first entry)

Mutant BCL-XL/BCL-2 associated cell death regulator #5.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

Mus sp. Synthetic.

W09817682-A1

97WO-US19175 17-0CT-1997;

30-APR-1998.

96US-0733505 18-OCT-1996;

(UNIW ) UNIV WASHINGTON

Korsmeyer SJ;

WPI; 1998-261422/23. N-PSDB; AAV27838 New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection

Claim 8; Page 73; 95pp; English.

mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding present invention describes mutant BAD (BCL-XL/BCL-2 associated cell The 

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                   phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
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100.0%; Pred. No. 4.5e-26;
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us-09-580-523-1.rapm

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB s Maximum DB s

Database

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Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 13, Appli
Sequence 13, Appli
Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APOPTOSIS TECHNOLOGY, INC.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: F137122
CURRENT APPLICATION NUMBER: PCT/USO0/11864
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VEF. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-184-168A-5
US-09-580-523-4
US-09-656-399-10
US-09-656-399A-10
US-09-716-395-20
US-09-656-399A-17
US-09-656-399A-17
                                                       US-09-716-395-26
US-09-656-399-15
US-09-656-399-16
PCT-US00-11864-3
US-09-580-523-3
PCT-US00-11864-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application PC/TUS0011864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                             Search time 239.36 Seconds
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US-09-410-372-1
US-09-456-357-32
US-09-580-523-1
US-08-883-731-2
US-08-410-372-7
US-09-410-372-7
US-60-197-873-16338
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                       GenCore version
Copyright (c) 1993 - 2000
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                                                                                                                                           October 9, 2001, 15:59:30
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Appli Appl Appl Appl Appl Appl Appl

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Gaps

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Score

Result

905 905 905 744 744 673

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us-09-580-523-1.rapm

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121 FVDSFKKGLPRPKSAGTATOMROSSSWTRVFOSWWDRNLGRGSSAPSO 168
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APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                              US-09-410-372-1; Sequence 1, Application US/09410372; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
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TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: amino acid
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Best Local Similarity 100.
Matches 168; Conservative
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; CLONE: 358673
US-09-410-372-1
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SOFTWARE: FASTSEC
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US-09-456-357-32
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121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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; Pred. No. 5.3e-71;
0; Mismatches 0;
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Pred. No. 5.3e-71;
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GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCY
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480440,428D2
CURRENT APPLICATION NUMBER: US/09/376,154
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                        Sequence 2, Application US/09375257;
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Olteradorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, EM.
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REPERENCE: 480140.42811;
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEO ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 905; Dest Local Similarity 100.0%; Pred. No. 5.3 Matches 168; Conservative 0; Mismatches
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Best Local Similarity 100.0%;
Matches 168; Conservative 0,
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US-09-375-257-2
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US-09-376-154-2
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLMAAQRYGRELRRMSDE 120
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121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSO 168
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                                                                                                                                                                                                                                APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc...
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 905; DB 18;
Pred. No. 5.3e-71;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURTENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation Cell Death
FILE REFERENCE: D6120
CURRENT APPLICATION NUMBER: US/08/883,731
CURRENT FILING DATE: 1997-06-27
EARLIER APPLICATION NUMBER: US 08/665,617
EARLIER FILING DATE: 1996-06-18
NUMBER OF SEQ ID NOS:,3
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                                                     121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                          121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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; OTHER INFORMATION: Protein encoded by the BBC6 gene.
US-08-883-731-2
                                                                                                                                                                              Sequence 21, Application US/09587473
GENERAL INFORMATION:
APPLICANT: Tahang, Hui
APPLICANT: Tahang, Hui
TITLE OF INVENTION: Protein Knockout Technology
FILE REFERENCE: 44574-5047-40
CURRENT APPLICATION NUMBER: US/09/587,473
CURRENT FILING DATE: 2000-06-05
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1168
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; Pred. No. 5.3e-71;
0; Mismatches 0;
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US-08-883-731-2
Sequence 2, Application US/08883731
; GENERAL INFORMATION:
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US-09-587-473-21
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Best Local Similarity
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US-09-587-473-21
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                                                          TITLE OF INVENTION: WIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND TITLE OF INVENTION: WETHOUS FOR MAKING AND USING THE SAME FILE REFERENCE: 3921-11-1
CURRENT APPLICATION NUMBER: US/09/456,357
CURRENT FILING DATE: 1999-12-08
EARLIER FILING DATE: 1999-05-17
EARLIER APPLICATION NUMBER: 09/087,195
EARLIER APPLICATION NUMBER: 09/087,195
EARLIER APPLICATION NUMBER: 08/378,507
EARLIER FILING DATE: 1998-05-29
EARLIER FILING DATE: 1995-01-26
EARLIER FILING DATE: 1995-01-26
EARLIER FILING DATE: 1994-05-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTING DATE: 1994-05-27
SEQ ID NO 3: SEQ ID NOS: 50

LENGTH: 168
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Xiao-Mai
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REPRENCE: A7483
CURRENT APPLICATION NUMBER: US/09/580,523
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
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100.0%; Pred. No. 5.3e-71;
ive 0; Mismatches 0;
Sequence 32, Application US/09456357
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 168; Conservative (
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US-09-580-523-1
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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; ORGANISM: Mus musculus PCT-US00-11864-3
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 16338
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                                                                                      US-60-197-873-16338
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PCT-US00-11864-3
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LENGTH: 162
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                                                  61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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                                                                                                       121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                          121 FVDSFKKGLPRPRSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Lal, Preet,
APPLICANT: Shah, Purvi
APPLICANT: Corley, Nail C
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESSE:
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 744; DB 18;
Pred. No. 6.4e-57;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/410,372 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                                                                                                                                                 Sequence 7, Application US/09410372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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85.1%;
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Matches 143; Conservative
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MEDIUM TYPE: Diskett
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; CLONE: 1683637
US-09-410-372-7
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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GENERAL INFORMATION:
APPLICANT: APOPTOSIS TECHNOLOGY, INC.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REPERENCE: F137122
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75.6%; Pred. No. 1.2e-48;
Live 12; Mismatches 23; Indels
121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                           APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordaro, Jean-Tyes
TITLE OF INVENTION: ESTS and Encoded Human Proteins
FILE REPERENCE: 81.021.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.4%; Score 673; DB 23;
100.0%; Pred. No. 7.2e-51;
ive 0; Mismatches 0;
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                                                                                                                                                                   Sequence 16338, Application US/60197873 GENERAL INFORMATION:
                                                                                                                                                                                                                                   APPLICANT: Bejanin, Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.
Matches 125; Conservative
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Matches 127; Conservative
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TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
TITLE OF INVENTION: PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
TOTHEL OF INVENTION: REGULATOR
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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                                                                                            158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
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TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
                                                                    121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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75.6%; Pred. No. 1.6e-48;
iive 12; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15871
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REFERENCE/DOCKET NUMBER: 965018
REFERENCE/DOCKET NUMBER: 965018
TELECPHONE: (314) 727-5188
TELEPHONE: (314) 727-518
TELEPHONE: (314) 727-518
TELEPHONE: (314) 727-518
TELEPHONE: (314) 727-518
TELEPHONE: CARRACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9715871 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 204 amino acids TYPE: amino acid
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Matches 127; Conserv
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STATE: MISSOURI
COUNTRY: USA
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PCT-US97-15871-1
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56 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 115
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                                                                                                                                                                                                                                                                             REGULATING APOPTOSIS, SCREENING FOR COMPOUNDS
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GENERAL INFORMATION:
APPLICANT: APOPTOSIS TECHNOLOGY, INC.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: F137122
CURRENT APPLICATION NUMBER: PCT/US00/11864
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATEUTIN VOR. 2.1
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                                      121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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75.6%; Pred. No. 1.2e-48;
Live 12; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 649; DB 1;
75.6%; Pred. No. 1.6e-48;
tive 12; Mismatches 23
                                                                                                                                                                                                                                                APPLICANT: Zhou, Xiao-Mai
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: AND METHODS OF MAKING AND
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: A7483
CURRENT APPLICATION NUMBER: US/09/580,523
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                         Application US/09580523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 127; Conservative
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Best Local Similarity 75.65
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus US-09-580-523-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
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Best Local Similarity
                                                                                                                                                                                                         Sequence 3, Applicat GENERAL INFORMATION:
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                                                                                                                                                                                 US-09-580-523-3
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TITLE OF INVENTION: PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COMPRESSORI
COMPRESSORI
LEP: 63105
COMPUTER READABLE FORM:
MEDIUM TYEE: PLOPPY disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                      MEDIUM TIPE: FIDDPY GISK
COMPUTER: IEBM PC compatible
COMPUTER: IEBM PC compatible
COMPUTER: IEBM PC compatible
COMPUTER: IEBM PC compatible
CURRENT APPLICATION DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R
REGISTRATION NUMBER: 6029-1938
REGISTRATION NUMBER: 6029-1938
TELEPOWNINICATION INFORMATION:
TELEPOWER (314) 727-5188
TELEPOWER (314) 727-5188
TELEPOREC CHARACTERISTICS:
LENGTH: 204 amino acid
STRANDEDNESS:
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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Search completed: October 9, 2001, 16:07:48 Job time: 498 sec

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LENGTH: 168
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Sequence 44485, A
Sequence 759, App
Sequence 4558, A
Sequence 7113, Ap
Sequence 7113, Ap
Sequence 5166, A
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Sequence 716, App
Sequence 1456, Ap
Sequence 54396, A
Sequence 53, Appl
Sequence 10232, A
Sequence 10233, A
Sequence 10233, A
                                                                                                (without alignments)
219.441 Million cell updates/sec
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44993, A
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Sequence 4499
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1 MFQIPEFEPSEQEDSSSAER.....RVFQSWWDRNLGRGSSAPSQ
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'Gqn2_6/ptodata/2/paa_YCT_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa_VUS06_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa_VUS08_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa_VUS09_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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PCT-US01-18569-2762
US-09-834-366-16338
US-09-922-378-3
US-09-758-466-716
US-09-758-466-716
US-09-760-466-716
US-09-760-466-716
US-09-760-461-53
US-09-760-461-53
US-09-760-485-1032
US-09-760-485-1032
US-09-760-485-1032
US-09-760-466-1147
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US-09-760-466-11485
US-09-750-473-759
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US-09-750-473-7513
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                                                                               October 9, 2001, 16:02:10
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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  985, App
3868, Ap
1172, Ap
49667, A
215089, A
215089, A
2178, Ap
8997, Ap
50030, A
45662, A
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38447, A
585, App
1761, Ap
8173, Ap
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Sequence 2762, Application PC/TUSO118569

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA133PCT

CURRENT APPLICATION NUMBER: 2001-06-07

PRIOR APPLICATION NUMBER: 60/209,467

PRIOR APPLICATION NUMBER: 60/209,467

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360.

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 168;
                                                                                                                                                                                                                                                                                                                        APPLICANT: Horne, william A. APPLICANT: Oltersdorf, Tilman A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: HOMAN BAD POLYPEPTIDES, ENCODING NUCLEIC TITLE OF INVENTION: ACIDS AND METHODS OF USE FILE REPERENCE: 480140, 42803 CURRENT APPLICATION NUMBER: US/09/922,378 CURRENT FILING DATE: 2001-08-03 NUMBER OF SEQ ID NOS: 15 SOFTWARR: FastSeQ for Windows Version 4.0 SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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PCT - USO1 - 08656 - 10231

PCT - USO1 - 08631 - 38680

PCT - USO1 - 08631 - 49667

PCT - USO1 - 14827 - 15089

PCT - USO1 - 14827 - 15089

PCT - USO1 - 14827 - 15089

PCT - USO1 - 08631 - 50030

PCT - USO1 - 08631 - 50030

PCT - USO1 - 08631 - 48762

PCT - USO1 - 08631 - 48762

PCT - USO1 - 08631 - 38447

US - 09 - 760 - 477 - 585

US - 09 - 760 - 477 - 585

US - 09 - 760 - 477 - 585

US - 09 - 760 - 477 - 1761

US - 09 - 760 - 477 - 1761

US - 09 - 760 - 477 - 1761

US - 09 - 760 - 477 - 1761

US - 09 - 760 - 477 - 1761
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100.0%; Score 905; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.6e-57;
Matches 168; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                             RESULT 1
US-09-922-378-2
; Sequence 2, Application US/09922378
; GENERAL INFORMATION:
 456
1209
1209
1647
620
832
1156
2911
3446
281
361
369
160
1160
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US-09-922-378-2
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LOCATION: (129)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 204;
                                                                                                                                                                                                                APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 434, Application US/09758466
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM036
CURRENT APPLICATION NUMBER: US/09/758,466
CURRENT PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PLILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                               ; Sequence 3, Application US/09922378
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-09-922-378-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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OTHER INFORMATION:
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LOCATION: (136)
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US-09-758-466-434
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SEQ ID NO 434
LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
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                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids MAME/KEY: SITE LOCATION: (146)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE

1. LOCATION: (174)

2. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-2762
                                                                                                                                                                                                                                                                                                               of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 FVDSFKKGLPRPKSAGTXTQMRQSSSWTRVFQSWWDRNLGXGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Deplain, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.082.REG
CURRENT PPLICATION NUMBER: US/09/834,366
CURRENT FILICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 864; DB 1; L. Pred. No. 5.2e-54; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16338, Application US/09834366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 Xaa equals any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.5%;
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Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 16338
LENGTH: 125
                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                   LOCATION: (169)
OTHER INFORMATION:
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                                                                                                                  NAME/KEY: SITE
LOCATION: (37)
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SEQ ID NO 2762
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LENGTH: 1401
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (178)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (206)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-466-716
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ON: (170) INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                          49 SHQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQ 108
                                                                                                                                  Gaps
                                                                                                                                                                                                   26 MFQIPEFEPSEQEDSSSAERGLGPSPAGRGP-----QAPASIIARPQASCGTPSPAG 77
                                                                                                                                  28;
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                                                                                       Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                    Score 223; DB 5; Length 14
Pred. No. 4.3e-09;
8; Mismatches 37; Indels
                                                                                                                                                                         1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLW---
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CURRENT APPLICATION NUMBER: US/09/758,466
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR PELING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 814
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 716, Application US/09758466
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                  Query Match 24.6%;
Best Local Similarity 45.1%;
Matches 60; Conservative 8
                                                                                                                                                                                                                                                                                                                                                      109 RYGRELRRMSDEF 121
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131 GYGRN-XELNDDF 142
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INFORMATION: Xaa
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OTHER INFORMATION NAME/KEY: SITE
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LOCATION: (199)
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    ; OTHER INFORMA
US-09-758-466-434
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OTHER INFO
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OTHER INFORMATION: Eukaryotic RNA polymerase II heptapeptide repeat proteins OTHER INFORMATION: domain identified by eMATRIX, accession number BL001152, p-val COTHER INFORMATION: 7.221e-09, raw score of 3.12 PCT-US01-08631-54396
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                                                   Gaps
                                                                                          19 ERGLGPSPAGDGPSGSGKHHRQAPGLL-WDASHQQEQPTSSS-----HHGGAGAVEIR 70
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Length 211;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC015
CURRENT APPLICATION NUMBER: US/09/760,476
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2602
SOFTMARE: Patentin Ver: 2.0
SEQ ID NO 1456
LENGTH: 123
                                              Indels
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GENERAL INFORMATION:
APPLICANT: Hyseq. Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                         127 KGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 102.5; DB 5; 62.9%; Pred. No. 1.1;
13.5%; Score 122.5; DB 5; 27.3%; Pred. No. 0.078; iive 15; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 PAGTEDDEGMGEEPSPFRGRSRSAPPN-----LW 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1456, Application US/09760476 GENERAL INFORMATION:
                     Best Local Similarity 27.3% Matches 44; Conservative
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SOFTWARE: CUSTOM
SEQ ID NO 54396
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Best Local Similarity 62.9
Matches 22; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LOCATION: (199).
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LOCATION:
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Sequence 10164, Application US/09902540

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Waxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15449)B
CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

LENGTH: 743
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTVA4
CURRENT APPLICATION NUMBER: US/09/760,461
CURRENT APPLICATION NUMBER: US/09/760,461
CURRENT APPLICATION APTE: 2001-01-16
FILO Application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 113
SCOTUMBER PATENTIN Ver. 2.0
SEQ ID NO 53
LENGTH: 535
      Length 1401;
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                                                                                                                                                                         75 SYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDS---
                                              Indels
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    DB 1;
Score 100.5; D
pred. No. 21;
8; Mismatches
  / Match 11.1%;
Local Similarity 26.0%;
hes 34; Conservative
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ORGANISM: Homo sapiens
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702 YHDSAPRPTSA 712
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US-09-760-461-53
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NAME/KEY: SITE
LOCATION: (236)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (344)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-760-461-53
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LOCATION: (344)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (236)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 PAKPEQGSSASR---PVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 PAKPEQGSSASR---PVPASRGGKTLCKGDRQAPPGPPARFPRPIWSASPPRAPRSSTPC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQA-----PGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQA-----PGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                              49;
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                  Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PU217

CURRENT APPLICATION NUMBER: US/09/760,485

CURRENT FILING DATE: 2001-01-16

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1477

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                                        57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 -----NSMPR-----LPTDLDVEGPWFRHYDFRQSCWVRAISQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVF---QSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVF---QSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                               Query Match 10.3%; Score 93.5; D
Best Local Similarity 25.0%; Pred. No. 23;
Matches 41; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 25.0%; Pred. No. 23;
Matches 41; Conservative 17; Mismatches
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25.0%;
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                                                                                                                                                                                                  (512)
                                                                                                                                                                  NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (256)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . LOCATION: (276)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-466-1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                 1235 HHLQQQRMAMMSQPQPQAFSPPPNVTASPSMDGVLAGSAMPQAPPQQFPYPA----NYG 1290
                                                                                                                                                                                                                                                                        86 MGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDAXASSEQASAQSEPSPAPPAQPQIYPXWRKLHISHDNIGGPKAKGPXRPTRATRPWSW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQM 141
                                                                                                                                       Gaps
                                                                                                                                                                                 37 HHRQAPGLLWDASHQQEQ------PTSSSHHGGAGAVEIRSRHSSYPAGTEDDEG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 SSSH-----AGAVEIRSRHS-SYPAGTE 81
                                                                                                                                       35;
                                                                                        Length 1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1147, Application US/09760466
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE NEFERENCE: PT259
CURRENT APPLICATION NUMBER: US/09/760,466
CURRENT FILIG DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapper SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.2%; Score 92; DB 5; Length 296; 25.1%; Pred. No. 16; ive 14; Mismatches 78; Indels
                                                                                        10.2%; Score 92.5; DB 5; Length 1 25.9%; Pred. No. 75; tive 12; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        1335 D----MKGWPSGNLARNGSFPQQ 1353
                                                                                                                                                                                                                                                                                                                                                              146 SWIRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                     37; Conservative
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    ; ORGANISM: Mus musculus
US-09-445-353C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                Best Local Similarity
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RRSSTST 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (231)
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LOCATION: (276)
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US-09-760-466-1147
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NAME/KEY: SITE
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LOCATION: (256
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                                                                                        Query Match
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LOCATION: (299)...(312)
OTHER INFORMATION: SMALL PROLINE-RICH PROTEIN SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00021A, p-value=1.911e-09, raw score
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠.
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: OTHER INFORMATION: RNA recognition motif. domain identified by PFam, accession

: OTHER INFORMATION: name rrm, E-value=0.074, PFam score of 14.6

PCT-US01-08656-10232
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GENERAL INFORMATION:
APPLICANT: Rosenfeald, michael G.
APPLICANT: Rose, David W.
APPLICANT: Torchia, Joseph
ITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
FILE REFERENCE: 6627-PAJ021
CURRENT APPLICATION NUMBER: US/09/445,353C
CURRENT APPLICATION NUMBER: PCT/US98/12263
PRIOR PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
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                                                                                                                                                APPLICAMT: Hyseq, inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR APPLICATION NUMBER: 09/720,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
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  -----NSMPR-----LPTDLDVEGPWFRHYDFRQSCWVRAISQ 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 RPKSAGTATQM-RQSSSWTRVFQSWWDRNLG--RGSSAPS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 54;
; Mismatches
                                                                                                           Sequence 10232, Application PC/TUS0108656 GENERAL INFORMATION:
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Matches 42; Conserv
                                                                 RESULT 12
PCT-US01-08656-10232
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63 GAGAVEIRSRHS-----SYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELR 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.1%; Score 91.5; DB 1; Length 1475; Best Local Similarity 33.3%; Pred. No. 93; Matches 41; Conservative 8; Mismatches 49; Indels 25
RESULT 15
PCT-UGO1-08631-44993

Sequence 44993, Application PC/TUS0108631

Sequence 44993, Application PC/TUS0108631

SEGNERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION:

CURRENT APPLICATION NOWEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 21272-049

CURRENT PELLING DATE: 2001-03-30

PRIOR FILING DATE: 2000-03-31

SPRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSCOM

SEQ ID NO 44993

LENGTH: 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NAME/KEY: misc_feature

: LOCATION: (1)...(1475)

: OTHER INFORMATION: Xaa = X or * as defined in Table 2

PCT-US01-08631-44993
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 RMS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, A
Sequence 2, A
Sequence 1, A
Sequence 12,
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Sequence 47,
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Sequence 55,
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Sequence 3,
                                                                                                                Search time 25.99 Seconds
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Sequence 5
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Sequence 1
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Sequence 3
Sequence 2
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-985-335-1

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US-08-333-565-2

US-08-61-479-2

US-08-733-505A-13

US-08-733-505A-13

US-08-733-505A-14

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US-08-733-505A-55

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US-08-733-505A-55

US-08-733-505A-55

US-08-733-505A-56

US-08-733-505A-56

US-08-733-505A-56

US-08-733-505A-56

US-08-733-505A-56

US-08-733-505A-58

US-08-733-505A-58

US-08-733-505A-58

US-08-733-505A-58

US-08-733-705A-78

US-08-733-705A-74

US-08-733-705A-74

US-08-733-74

US-08-74

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                                                                                                                                                                                                                                                                                                                               197339 segs, 20590346 residues
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1 MFQIPEFEPSEQEDSSSAER....
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Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                           US-09-580-523-1
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Match 1
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APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 168;
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKÉT UNBER: 31,815
REFERENCE/POCKÉT UNBER: 9-ID 1929
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON:
TELECOMMUNICATION ON:
STELECOMMUNICATION ON:
STELECOMMUNIC
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1larity 100.0%; Pred. No. 4.4e-86;
Conservative 0; Mismatches 0;
                 US-09-227-420-3

US-09-227-420-3

US-09-026-587-1

US-08-986-217-6

US-08-986-217-6

US-08-661-479-26

US-09-661-479-26

US-09-661-479-26

US-09-026-587-4

US-09-227-420-4

US-09-351-215-13

US-09-356-242-13

US-09-356-242-13

US-09-356-242-13

US-09-356-217-420-4

US-09-356-17-17-18-18

US-09-226-012-4

US-08-333-565-17

US-08-681-17-18-18
                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 168 amino acids TYPE: amino acid
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16
380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: United Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 168; Conserv
  92122
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US-08-717-123-2
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120

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121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                        NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                              32606
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US-08-985-335-7
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                      61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAORYGRELRRMSDE 120
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                                                                          121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 905; DB 3;
100.0%; Pred. No. 4.4e-86;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                        Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.(
Matches 168; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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MEDIUM TYPE: Diskett
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CLONE: 358673
US-08-985-335-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
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                                                                                                                                                                                      US-08-985-335-1
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54 QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xudong, Yin TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 LRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preetti
APPLICANT: Shah, Purvi
APPLICANT: CAILEY, Neil C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 751; DB 1;
Pred. No. 3.3e-70;
                                                                                                                                                               ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/POCKET NUMBER: CL-8
TELECHONICATION INFORMATION:
TELEPHONE: (352) 375-8100
INFORMATION FOR SEO ID
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/08985335
; Patent No. 6080847
; Sequence 2, Application US/08665617
; Patent No. 5663316
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84.0%;
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.7%; Score 649; DB 1; Length 204; Best Local Similarity 75.6%; Pred. No. 1.4e-59; Matches 127; Conservative 12; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/O8661479
Patent No. 5834209
GENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
TUMBER OF SEQUENCES:
ORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STARET: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Deduced amino acid sequence of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFRENCE/DOCKET NUMBER: 15726
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2402
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                         l: 204 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CTHER INFORMATION: ; CTHER INFORMATION: ; CTHER INFORMATION: CUS-08-333-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino & STRANDEDNESS:
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Fatent No. 5622852
GENERAL INFORMATION:
FAPLICANT: KORSMETE, Stanley J.
TITLE OF INVENTION: BGL-X/BGL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
TITLE OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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Pred. No. 1.8e-69;
0; Mismatches 25; Indels
                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: DISKETTE
COMPUTER: DISKETTE
COMPUTER: DISKETE
COMPUTER: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNDBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELEPHONE: 650-885-0555
TELEPHONE: 650-885-0555
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.2%;
Best Local Similarity 85.1%;
Matches 143; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank
                                                                                   Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: 1683637
US-08-985-335-7
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LIBRARY: GenBa
                                                                                                                                  USA
                                                                                                                                                  ZIP: 94304
                                                                                                            STATE: C
COUNTRY:
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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                                                                                                                                                                                                                                                                                                 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                           1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12. Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                         Query Match 71.7%; Score 649; DB 2; Length 204; Best Local Similarity 75.6%; Pred. No. 1.4e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.4%; Score 646; DB 2; Length 204; 75.0%; Pred. No. 2.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
                                                                                                                                                                                                                                                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.96
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7733 FORSYTH BLVD., SUITE 1400
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NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6188
ITELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 13;
         SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
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                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-733-505A-12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 126; Conserv
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: MISSOURI
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                                                     TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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US-08-733-505A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE S.
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 71.7%; Score 649; DB 2; Length 204; Best Local Similarity 75.6%; Pred. No. 1.4e-59; Matches 127; Conservative 12; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Deduced amino acid sequence of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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APPLICATION NUMBER: US/08/733,505A FILING DATE:
CLASSIFICATION: 530
ATTONNEX/AGENT TWANTER:
NAME:
FILING DATE: 31-OCT-1994

ATTORNEY/AGENT INCRMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPROMUNICATION INFORMATION:
TELEPRONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
'TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-5188
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..204
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
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CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-733-505A-1
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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Patent No. 5856445
GENERAL INFORMATION:
APPLICAT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BELLATORE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic TITLE OF INVENTION: Acids and Methods of Use NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESSE: Campbell and Flores STREET: Campbell and Flores STREET: Campbell and STREET: Campbell and STREET: Campbell and STREET: Campbell and STREET: California COUNTRY: United States ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.4%; Score 646; DB 2; 75.0%; Pred. No. 2.9e-59; tive 13; Mismatches 23
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CORRESPONDENCE ADDRESS:
CORRESCEDE: HOWELL, & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERRICE/DOCKET NUMBER: 9-ID 1929
TELECOMMUNICATION INFORMATION:
  Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 204 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.09
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-717-123-3
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                                                                   HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
                                                                                          61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 646; DB 2; Length 204; 75.0%; Pred. No. 2.9e-59; Live 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35.197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.4% Best Local Similarity 75.0% Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                            RESULT 9
US-08-733-505A-13
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US-08-717-123-3
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Gaps

23; Indels

COMPUTER READABLE FORM

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Length 204;

Length 59;

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TELEFAX: (314) 727-6092 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 59; Conservative
                                                                        59 amino acids
                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                             amino acid
                                                                                             TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
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US-08-733-505A-57
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                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-733-505A-55
Sequence 55, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.0%; Score 643; DB 2; Best Local Similarity 74.4%; Pred. No. 5.9e-59; Matches 125; Conservative 14; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                      FILING DATE:
CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: HOLLAND, DONALD R.
• REGIESTRATION NUMBER: 35,197
REFERENCE/COCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
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                                                                                                                                1 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEF 59
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                                                                                                                                                                                                                                                                           Sequence 56. Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.4%; Score 311; DB 2; Length 59; 98.3%; Pred. No. 2e-25;
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
34.7%; Score 314; DB 2; 100.0%; Pred. No. 9.8e-26; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.35
Matches 58; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 530
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL. XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADBRESS:
STREET: 7733 FORSYTH BLVD., SUITE 1400
COTTY: ST. LOUIS
               GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

ATTILE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

KUNBAR OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: MISSOURI

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
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PPLICATION NUMBER: US/08/733,505A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 57, Application US/08733505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-57
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099479 human corters
099479 human nogrets
068831 human cytom
06494 feline immu
066944 feline immu
08553 feline immu
08553 feline immu
08558 feline immu
080558 feline immu
080558 feline immu
080558 feline immu
080558 potato viru
08105 potato viru
085105 potato viru
085115 potato viru

09YL74 066931 066944 066944 066944 085553 09H285 09H285 09H285 09H285 09H285 09H285 09H285 09H285 09H285 09H286 09H28 0

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Ottilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G., Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T., J. Biol. Chem. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=97083574; PubMed=8929532; MEDLINE=97083574; PubMed=80.7C.; Mapp U.R., Reed J.C.; "Bcl-2 targets the protein kinase Raf-1 to mitochondria."; Cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 145; DB 4; Best Local Similarity 100.0%; Pred. No. 3.4e-13; Matches 26; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
  Homo sapiens (Human).
  \begin{array}{c} \mathbf{c} \ \mathbf{
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01-JAN-1998
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09h108 homo sapien
098808 yam mosaic
09e17 turnip mosa
09u749 trypanosoma
09hu59 pseudomonas
074309 schizosacch
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Q66962 feline immu
Q9eae6 lettuce mos
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Copyright (c) 1993 - 2000 Compugen Ltd.
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MEDLINE-96370790; Pubmed-8774686;
Aleman M.E., Marcos J.F., Brugidou C., Beachy R.N., Fauquet C.;
"The complete nucleotide sequence of yam mosaic virus (Ivory Coast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ417L20.1 (CYSTEINE-RICH SECRETORY PROTEIN 3 (CRISP-3, SGP28))
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Pred. No. 6.8;
3; Mismatches 5; Indels
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL121974; CAC19654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22912 MW; F80D707EE0D81A2B CRC64;
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Last annotation update)
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Arch. Virol. 141:1259-1278(1996).
-!- MILLARITY: TO HELICASE C-TERMINAL DOMAIN.
EMBL; U42996; AAC55551.1;
InterPro; IPR001410;
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                                                                                                                                                                          203 AA.
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Pred. No. 1.2;
5; Mismatches
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180 QSASWTRIIQSWWDRNLGKGGSTPSQ 205
                                                                                                                                                                       PRT;
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SMART; SM00487; DEXDC; 1.
ATP-binding; Helicase.
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39.3%;
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50.0%;
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Best Local Similarity 39.3'
Matches 11, Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=41460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Q9H108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSU S.Y., Hsueh A.J.W.;
"Interference of BAD (Bc1-xL/Bc1-2-associated death promoter)-induced apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
MO1. Endocrinol. 11:1858-1867(1997).
EMBL; AF003523; AAC53374.1; --
SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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EMBL, AR031227, AAC15100.1; -
EMBL, AF279910; AAF91427.1; -
SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90194755; PubMed-9535132; D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator Bad the rat brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 76.9%; Pred. No. 3.9e-10;
Matches 20; Conservative 3; Mismatches 3; Indels
                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER.
                                                                                 205 AA.
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                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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BAD OR BAD-ALPHA.
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NCBL_TaxID-5693;
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                                                                                                                         Turnip mosaic virus (strain Japanese) (TuMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                 Kundu A.K., Obshima K., Sako N., Yaegashi H.;
"Cross-reactive and major virus-specific epitopes are located at t
N-terminal halves of the cylindrical inclusion proteins of turnip
mosaic and zucchini yellow mosaic potyviruses.";
Arch. Virol. 145:1437-1447(2000).
EMBL; AB030276; BAB16312.1;
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                                                                                                                                                                                                                                                                                                           Score 54; DB 14; Length 731;
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                                                                        (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TYPPANOSOMA CTUZI.
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Pred. No. 3.5;
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38.9%;
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99 KTFASWWNHQLSRGFTIP 116
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Best Local Similarity 38.9
Matches 7; Conservative
| | : | | | : | : |
35 FQTWWDRQIVSGRTIP 50
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                                                       PRELIMINARY;
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Best Local Similarity
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                                                                                                                                         Potyvirus.
NCBI_TaxID=12230;
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01-MAR-2001
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Gaps
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10.NOV-1998 (TrEMBLrel. 08, Last sequence update)
11.NOV-1998 (TrEMBLrel. 16, Last sequence update)
11.NAR-2001 (TrEMBLrel. 16, Last annotation update)
12. PLARY-2001 (TREMBLrel. 16, Last annotation update)
13. Schizosacharomyces pombe (Fission yeast).
14. Schizosacharomycetales; Schizosaccharomycetales; Sch
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101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
107-COMPONENT RESPONSE REGULATOR NTRC.
NTRC OR PA5125.
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476 AA
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INTERPO; IPR001789; -.
INTERPO; IPR002199; -.
INTERPO; IPR002197; -.
Pfam; PF00072; response_reg; 1.
Pfam; PF00072; response_reg; 1.
PROSITE; PS00676; SIGMA54_INTERACT_1; 1.
PROSITE; PS00688; SIGMA54_INTERACT_2; 1.
PROSITE; PS50045; SIGMA54_INTERACT_2; 1.
PROSITE; PS50045; SIGMA54_INTERACT_3; 1.
PROSITE; PS50045; SIGMA54_INTERACT_3; 1.
SEQUENCE 476 Aa; 52753 WW; 7DEBD71BA300
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PROSITE; PS00678; WD_REPEATS; UNKNOWN_1
                                                                                                             Created)
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PRT;
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Nature 406:959-964(2000).
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Best Local Similarity 38.1
Matches 8; Conservative
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Best Local Similarity
Matches 9; Conserv
                                                                 SEQUENCE FROM N.A.
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                          NCBI_TaxID=11673;
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"The cylindrical inclusion gene of Turnip mosaic potyvirus encodes a pathogenic determinant to the Brassica resistance gene TuRB01.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
EMBL; AF169561; AAF89676.1;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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63;
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SMART; SM00320; WD40; 1.
Repeat; WD repeat.
SEQUENCE 807 Aa; 90432 MW; B8BFB73852EB7B45 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                  Score 53; DB 3
Pred. No. 16;
1; Mismatches
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Pred. No. 63;
2; Mismatches
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PF00767; Poty_coat; 1.
PF00851; Peptidase_C6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Helicase.
SEQUENCE 3164 AA; 357537 MW;
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PRINTS; PR00966; NIAPOTYPTASE.
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Feline immunodeficiency virus.
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
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InterPro; IPR001254; -.
InterPro; IPR001410; -.
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InterPro; IPR002540; -
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624 SSSWLRVSEGWW 635
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089177
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J. Virol. 68:2230-2238(1994).

EMBL; U02418; AAA18042.1;
                                                                                                                                                                                                                                                                   Gaps
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           Watari T., Tsujimoto H., Hasegawa A.;
"Genetic heterogeneity of ENV gene of Feline immunodeficiency virus obtained from several districts in Japan.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010397; BAA31442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=USILBRNY03B;
MEDLINE=94187063; Pubmed=8139008;
SOGOTA D.L., Shpaer E.G., Kitchell B.E., Dow S.W., Hoover E.A.,
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Nishimura Y., Goto Y., Hai P., Momoi Y., Endo Y., Mizuno T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 14; Length 224; Pred. No. 9;
                                                                                                                                                                                                                           14; Length 208;
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                                                                                                                            1 1 208 208 208 W, CD2AAECE2CEA777B CRC64;
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Last annotation update)
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 8.3;
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01-MAY-1997 (TrEMBLrel. 03, Last seq
01-JAN-1999 (TrEMBLrel. 09, Last ann
ENV PROTEIN (FRAGMENT).
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25902 MW;
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56.2%;
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224 AA;
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Search completed: October 9, 2001, 15:54:58
Job time: 193 sec
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Best Local Similarity 25.5
Matches 12; Conservative
 Bacteriophage phi-C31
                                              SEQUENCE FROM N.A. STRAIN-NORWICH STOCK;
                                                                                              SEQUENCE FROM N.A.
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                                   STRAIN-LP9;
MEDLINE-96406913; PubMed-8811000;
PECOTATO M.R., Tomonaga K., Miyazawa T., Kawaguchi Y., Sugita S., Tohya Y., Kai C., Etcheverrigaray M.E., Mikami T.;
"Genetic diversity of Argentine isolates of feline immunodeficiency virus.";
J. Gen. Virol. 77:2031-2035(1996).
EMBL: D84497; BAA12687.1;
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                                                                                                                                                              Score 51; DB 14; Length 242; Pred. No. 9.7;
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Pred. No. 11;
); Mismatches 7; Indels
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242 AA; 28035 MW; 3CF75A2F5E37DBF0 CRC64;
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
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Last annotation update)
Retroid viruses; Retroviridae; Lentivirus.
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56.2%;
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56.2%;
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity
                           SEQUENCE FROM N.A.
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         NCBI_TaxID=11673;
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Viruses:
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Gaps
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10719;
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                                                                                                                                                                                                                                                                                                                  STRAIN-NORWICH STOCK;
MEDLINE-99162580; PubMed-10051617;
MEDLINE-99162580; PubMed-10051617;
Hendrix R.W., Smith M.C.M., Burns N., Ford M.E., Hatfull G.F.;
"Evolutionary relationships among diverse bacteriophages and prophages: all the world's a phage.";
proc. Natl. Acad. Sci. U.S.A. 96:2192-2197(1999).
EMBL, AJ006589; CAA07120.1;
SEQUENCE 362 AA; 38359 WW; 878AE3DA5E53DBCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%; Score 51; DB 9; Length 362; 25.5%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                       Smith M.C.M.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
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OM protein - protein search, using sw model

; Search time 24.69 Seconds
(without alignments)
518.320 Million cell updates/sec October 9, 2001, 15:57:35 Run on:

Title:

09-580523-1A 902 1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168 Perfect score:

Sequence:

Scoring table:

219241 seqs, 76174552 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

;		ap ,			SUMMARIES	
Result No.	Score	Query Match	Length	DB	OI.	Description
1	645	71.5	204	7	A55671	bad protein - mous
7	94.5	10.5	1729	7	T18396	erythrocyte membra
٣	93	10.3	1300	7	T03166	=
4	. 91	10.1	834	7	T42702	hypothetical prote
ທ	91		2248	7	A35938	
9	90		2237	7	T45115	N-type calcium cha
7	06	10.0	2339	7	A42566	omega-conotoxin-se
8	89.5	6.6	393	~	JC5614	RNB6 protein - rat
6	88.5	•	336	7	T30757	Q,
10	88.5	•	449		A41520	chromogranin A pre
11	87	•	222	7	T43500	
12			1077	7	A44067	Ω
13	86.5		1647	7	845252	SNF2beta protein -
14	86.5	9.6	2715	~	T13049	eyelid - fruit fly
15	98	•	270	-	WJMS13	homeotic protein H
16	86		343	7	T05221	hypothetical prote
17	98	9.5	420	7	B38104	LFY floral meriste
18	98	•	646	П	S15901 .	chromogranin B pre
19	84.5	9.4	134	~	154810	pHL ElF1 - human
20	84.5	9.4	1323	7	T00037	hypothetical prote
21	84.5	9.4	1392	7	T51947	probable transcrip
22	84.5	9.4	1562	~	T29146	hypothetical prote
23	84		270	Н	WJHU1C	homeotic protein H
24	84	9.3	313	7	A28444	filaqqrin precurso
25	84	9.3	380	7	S51797	vasodilator-stimul
56	84	9.3	381	~	S16506	hypothetical prote
27	84	•	542	N	A44358	zyxin - chicken
28	83.5	9.3	380	7	T24786	pr
29	83.5	9.3	625	7	A34615	profilaggrin - rat

probable potassium	endozepine related	hypothetical prote	polycomb protein e	probable secretory	heterogeneous ribo	subtilisin-type al	cyclin T - fruit f	myosin-IA - Acanth	microtubule-associ	LFY floral meriste	hypothetical prote	mannan endo-1,4-be	hypothetical prote	period protein Per	filaggrin - mouse	
138465	T49431	S07132	T13154	T36677	A33616	н83736	T13033	T32734	A54602	A38104	T28770	T10748	T00329	T13955	A31488	
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1159	337	886	2023	523	558	792	1097	1215	1734	424	539	1021	1095	1115	254	
9.3	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.7	9.1	9.1	9.1	9.1	9.0	
83.5	83	83	83	82.5	82.5	82.5	82.5	82.5	82.5	82	82	82	82	82	81.5	
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45	

## ALIGNMENTS

Н	
ESULT	55671

RESULT 1
A55671
bad protein - mouse
C;Species: Was musculus (house mouse)
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C;Accession: A55671
E;Yang E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Reference number: A55671; MUID:95136361
A;Accession: A55671
A;Accession: A55671
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRAN
A;References: GB-L37296; NID:9639778; PIDN:AAA64465.1; PID:9639779
C;Keywords: heterodimer

Gaps ; 9 Length 204; 24; Indels 71.5%; Score 645; DB 2; 75.0%; Pred. No. 1.1e-45; tive 12; Mismatches 24; Query Match 71.5% Best Local Similarity 75.0% Matches 126; Conservative

3

1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60 43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97 g ò

HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120

61 ò q

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RESULT

Tryphocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fr. 5pecies: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: 15-oct-1999 #sequence\_revision 15-oct-1999 #text\_change 09-Jun-2000 C; Accession: T18396 #sequence\_revision 15-oct-1999 #text\_change 09-Jun-2000 C; Accession: T18396 B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, Cell 82, 77-87, 1995 A; 1

11;

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C;Species: Homo saplens (man)
C;Date: 14-Dec-1990 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Date: 14-Dec-1990 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: A35938
R;Gan, S.Q.; McBride, O.W.; Idler, W.W.; Markova, N.; Steinert, P.M.
Biochemistry 29, 9432-9440, 1990
A;Title: Organization, Structure, and polymorphisms of the human profilaggrin gene.
A;Reference number: A35938; MUID:91064347
A;Recession: A35938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1q21-1q21
S. Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology
C; Keywords: EF hand; epidermis; polymorphism; tandem repeat
F; 246-569/Region: filaggrin repeat
F; 570-893/Region: filaggrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSR----HSSYPAGTEDDE-GMGEEPSP----FRGRSRSAPP-----NLWAAQRY--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 GRELRRMXDEFVDSFKK------GLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---RELGK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQARSSAGERHGSHHQQSADSSRHSGIGHGQASTAVSDSGHRGYRGSQASDNEGHSEDSD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RGRSRGGSGRSGSFLYOVSTHEOSES 258
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                     13 EDSSSAERGLGPSP---AGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI 69
                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-2248 <GAN>
                                                                                                                                                                                                                                                                             Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels
                                                                                                                                                                                                                                                                                                                                     51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSR-----
                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 213-834 <AA2>
A;Cross-references: EMBL:AL137336
A;Experimental source: adult testis; clone DKF2p434B239
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
18;
                                                                                                                                                                                                                                                                                  Score 91; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPPAGV---
                                                                                                                                                                                                                                                                                                             Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:FLG
A;Cross-references: GDB:119912; OMIM:135940
                                                                                                                                                                                                  A; Note: DKFZp434F117.1; DKFZp434B239.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 PNLWAAQRYGRELRRMXDEFVDS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1074-1397/Region: filaggrin repeat
F;1573-1896/Region: filaggrin repeat
                                                                                                                                                                                                                                                                                  10.1%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%;
26.6%;
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                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity 26.69
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: J02929
A; Reference number: 223029
                                                                                                                                                                                                                                                                                                             Best Local Similarity
                          A; Accession: T46502
                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 G 373
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C;Accession: T03166
R;Ensser, A; Pflanz, R; Pleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: 214840; MUID:97404659
A;Accession: T03166
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1300 < CNS>
A;Residues: 1-1300 < CNS>
A;Cross-references: EMBL;AF005370; NID:92337967; PIDN:AAC58118.1; PID:92338034
C;Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein DKFZp434F117.1 - human (fragment)
N;Alternate names: hypothetical protein DKFZp434B239.1
C;Speciaes: Homo sapiens (man)
C;Speciaes: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C;Accession: T42702; T46502
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A;Reference number: 22234
A;Accession: T42702
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-834 <AAA>
A;Cross-references: RMBL:AL133028
A;Experimental source: adult testis; clone DKFZp434F117
R;Poustkå, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
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                                                                                                                                                                                                                                                                                                             PSGNESSPSEKLPQGPTPETTKETPESSLLHAFVSPPRLRRFLPW---HKFKEQWKAQHG 982
                                                                                                                                                                                                                                                                                  GGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRY------ 110
                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 PEGEGPERPEGPEGPEGPEGPEGPEGPEGPERDSP----DGPGAQEGPEGPEG 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                             Gaps
                                                                                                                                                                          9 PSEQEDSSSAERGLGPSP--AGDGPSGSGKHHRQAPGLL----WDASHQGEQPTSSSHH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                     --GRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PEFEPSEQEDSSSAERGLGP-SPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGG
                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                     Length 1729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.3%; Score 93; DB 2; Length 1300; Best Local Similarity 29.0%; Pred. No. 6.7; Matches 31; Conservative 6; Mismatches 56; Indels
                                                                                                                          Indels
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                                                                                                                          :99
                                                                        DB 2;
                                                     10.5%; Sco...
21.6%; Pred. No. o...
...a. 23; Mismatches
                                                                  Query Match
Best Local Similarity 21.6'
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1087 SVEKTPOOTWWEAN 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QSWWDRN 158
A; Note: var-2
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hypothetical protein 155R - Molluscum contagiosum virus 1
N.Alternate names: MC155R
C.Specias: Molluscum contagiosum virus 1
C.Specias: Molluscum contagiosum virus 1
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C.Accession: T30757
R.Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A.Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
A.Reference number: Z20876; MUID:96325459
A.Accession: T30757
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-336 <SEN>
A.Residues: 1-336 <SEN>
A.Residues: 1-356 <SEN>
A.Cocession: C.Genetics:
A.Note: MC155R
                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Sep-1997 #sequence_revision 17-oct-1997 #text_change 05-Nov-1999
C;Date: 23-Sep-1997 #sequence_revision 17-oct-1997 #text_change 05-Nov-1999
C;Date: 23-Sep-1997 #sequence_revision 17-oct-1997 #text_change 05-Nov-1999
C;Date: 23-Sep-1997 #sequence 0. M.; Tabuchi, K.
Biochem. Biophys. Res. Commun. 237, 307-312, 1997
A;Title: Differential display cloning of a novel rat cDNA (RNB6) that shows high expr
A;Reference number: JC5614
A;Mocession: JC5614
A;Mo
                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-393 <OHT>
A;Cross-references: GB:U70211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462
A;Experimental source: brain
C;Comment: This protein belongs to Ena/VASP family member, and is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HSSYPAGTEDDEGMGEEP--SPFRG-RSRSAPPNLWAAQRYGRELRRMXD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 LLAKRRKAASQTDKPADRKEDENQTEDPSTSPSPGSRATSQPPNSSEAGRKPWERSNSVE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RSRSAPPNLWAAQRYGRELR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDAS-----AGSSPSGTSKS-----DANR-----ASSGGGGGLMEEMNK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQEDSSSAERGLGPSPAGDGPSGSGKHHRQA-PGLLWDASHQQEQPTSSSHHGGAGAVE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 EDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RMXDE-FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 393;
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; Pred. No. 3.6;
16; Mismatches
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28.28;
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Best Local Similarity 30.1%
Matches 52; Conservative
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Best Local Similarity
Matches 40; Conserva
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                                                                                                                                                                                                                                                                                          R.Williams, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; Mcd Science 257, 389-395, 1992
A.Fille: Structure and functional expression of an omega-conotoxin-sensitive human N-typ A;Reference number: A42566; MUID:92335886
A;Accession: T45115
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Schence 257, 389-395, 1992
A;Title: Structure and functional expression of an omega-conotoxin-sensitive human N-typ
A;Reference number: A42566; MUID:92335886
                                                                                                                                                                        N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively
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ص
                                                                                                                                                                                                  C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-2237 <WIL>
A; Cross-references: EMBL: M94173; NID:g179759; PIDN: AAA51898.1; PID:g179760
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 -SHQQEQPTSSSHHGGAGAV-EIRSRHSSYP-AGTEDDEGMGEEPS-PFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description: calcium influx Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: IMR32, hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:109168)
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2237;
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A.Status: preliminary: not compared with conceptual translation A:Molecule type: nucleic acid
A:Residues: 1-2339 <WILD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPSEQED----SSSAERGLGPSPA-----GDGPSGSGKHHRQAPGLLWDA-
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; Pred. No. 21;
16; Mismatches 3
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1larity 30.8%; Pred. No. 22;
Conservative 16; Mismatches
259 SHGWARTSTGRRQGSRHDQAQDS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.8%;
Matches 36; Conservative 16
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                           Accession: T45115
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C; Function:
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A;Title: Nature of the pH-induced conformational changes and exposure of the C-termin A;Reference number: S38976; MUID:94063061
A;Accession: S38976
                                                                                                                                                                                                                                                                                             C;Comment: Chromogranin A is the major protein of bovine chromaggin granules. C;Comment: Chromostatin activity has been demonstrated from proteolytic fragments C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFzp586G1721.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T45500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 LLAKRRKAASQSDKPAEKKEDESQMEDPSTSPSPGTRAASQPPNSSEAGRKPWERSNSVE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 EVEKSDEDSDGDRPOASPGLGPGP-----KVEEDNOAPG-----EEEEAPSNAH-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXD--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, December 1999
A; Reference number: 222515
A; Accession: T43500
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDAS------GGSSPSGTSKS-----DANR-----ASSGGGGGLMEEMNK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 EFEPSEQE---DSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 EDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F)19-449/Product: chromogranin A #status experimental <MAT>F)142-161/Product: chromostatin #status predicted <MAT3>F)266-312/Product: pancreastatin #status experimental <MAT2>F)365-50/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 WEEAEAREKAVPEEESPPTAAFKAPPSLGNKETQRAAPGW 270
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-18/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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; Pred. No. 5;
19; Mismatches
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Best Local Similarity 24.4%;
Matches 39; Conservative 19
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                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 19-26; 266-272 < YOO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 41; Conserv
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A; Residues: 1-222 <AAA>
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                                                                                                                                                               A;Status: preliminary
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chromogranin A precursor [validated] - bovine
N;Alternate names: pituitary secretory protein I; secretory protein I
N;Contains: chromostatin; pancreastatin
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C;Accession: A41520, A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976
R;Iacangelo, A.L.; Grimes, M.: Eiden, L.E.
Mol. Endocrinol. 5, 1651-1660, 1991
A;Title: The bovine chromogranin A gene: structural basis for hormone regulation and gen A;Title: The A1520; MUID: 92140395
A;Accession: A41520
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-111, 'T', 113-190, 'Y', 192-253,'P', 255-378,'R', 380-449 <AHN>
A; Residues: 1-111, 'T', 113-190,'Y', 192-253,'P', 255-378,'R', 380-449 <AHN>
A; Cross-references: GB:M16971; NID:g163727; PIDN:AAA30765.1; PID:g163728
A; Note: the authors translated the codon CGG for residue 391 as Gln
R; lacangelo, A.; Affolter, H.U.; Eiden, L.E.; Herbert, E.; Grimes, M.
Rature 323, 82-66, 1986
A; Title: Bovine chromogranin A sequence and distribution of its messenger RNA in endocri
A; Reference number: A24175; MUID:86311345
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A. Molecule type: protein

B. Mesaidues: 19-34, X', 38-39-111;134-139 <BA2>

R. Mesaidues: 19-34, X', 3-38-97-111;134-139 <BA2>

R. Watkinson, A.; Joensson, A.C.; Davison, M.; Young, J.; Lee, C.M.; Moore, S.; Dockray, Biochem. J. 276, 471-479, 1991

A. Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and ad A; Reference number: S15847; MUID:91264803

A. Accession: S15847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: A24175
A;Molecule type: mRNA
A;Rossidues: 1-153, PO',156-158, R',160-190, Y',192-253, P',255-449 <IA2>
A;Cross-references: GB:X04298; NID:g217; PION:CAA27841.1; PID:g218
R;Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ishida, K.; Makk, G.; Angwin, P.; Chang, D.;
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A; Residues: 266-310, 'H', 312-318,'K', 320-331 <WA2>
A; Residues: 266-310, 'H', 312-318,'K', 320-331 <WA2>
A; Note: 311-Arg and 319-Glu were also found
R; Watkinson, A; Rogers, M; Dockray, G.J.
Biochem. J. 295, 649-654, 1993
A; Title: Post-translational processing of chromogranin A: differential distribution of A; Reference number: S39016; MUID:94059013
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A;Residues: 303-331 <WAT>
R;Benedum, U.M.; Baeuerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.;
EMBO J. 5, 1495-1502, 1986
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A; Residues: 266-312 < NAK>
R; Barbosa, J.A.; Gill, B.M.; Takiyyuddin, M.A.; O'Connor, D.T.
Endocrinology 128, 174-190, 1991
A; Title: Chromogranin A: posttranslational modifications in secretory granules.
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Regul. Pept. 25, 207-213, 1989
A;Title: Isolation and characterization of bovine pancreastatin.
A;Reference number: A60306; MUID:89331945
A;Accession: A60306
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09-580523-la.rpr

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National manes: homeotic protein Hox 1.3; homeotic protein m2
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (soft): A30761; A30763
R; Fibi, M.; Zink, B.; Kessel, M.; Colberg-Poley, A.M.; Labeit, S.; Lehrach, H.; Gruss Development 102, 349-359, 1988
R; Fibi, M.; Zink, B.; Kessel, M.; Colberg-Poley, A.M.; Labeit, S.; Lehrach, H.; Gruss Development 102, 349-359, 1988
A; Reference number: A30340; MUID:88328807
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: Muscule type: Muscul
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C; Species: Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C; Accession: T13049
C; Accession: T12049
C; Accessio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TSSSHHGGAGAVEIRSRHSSYPAGT-EDDEGMGEE-----PSPFRGRSRSAPPNL 104
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                                                                                                                                                                               9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH---RQAP-GLLWDASHQQEQPTSSSHHGGA 64
                                                                                                                                                                                                                                                                                                  30 PSPGPSPGSAHSMMGPSP---GPPSAG--HPIPTQGPGGYPQDNMHQMHKPMESMHEKGM 84
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                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 SDDPRYNQMKGMGMRSGGHAGMGPPPSPMDQHSQGYPSPLGGSE 128
                                                            55;
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Best Local Similarity 25.8%; Pred. No. 50;
Matches 41; Conservative 11; Mismatches
                                                                  9; Mismatches
      Pred. No.
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C;Function:
29.8%;
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Best Local Similarity 29.8 Matches 31; Conservative
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A; Molecule type: DNA
A; Residues: 1-270 <ODE>
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                        Serine-rich protein hairless - fruit fly (Drosophila melanogaster)

NAlternate names: 109K basic protein H
C;Species: Drosophila melanogaster
C;Date: 10-Jun-1993 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999
C;Accession: A44067; A58929; S33412; S24639
R;Bang, A.G; Posakony, J.W.
Genes Dev. 6, 1752-1769, 1992
A;Title: The Drosophila gene Hairless encodes a novel basic protein that controls altern
A;Reference number: A44067, MUID:92387549
A;Reference number: A44067, MUID:92387549
A;Residues: 19-1077 CBAN>
A;Residues: 19-1077 CBAN>
A;Residues: 19-1077 CBAN>
A;Reference extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)
B;Preiss, A. Residues: A58929
A;Reference number: A58929
A;Reference number: A58929
A;Recession: A58929
A;Recession: A58929
A;Recession: A58929
A;Recession: A58929
A;Recession: A58929
A;Reference number: A58929
A;Recession: A58929
A;Reference number: S33412; MUID:93041287
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C;Species: Homo sapiems (man)
C;Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C;Accession: $45252
C;Accession: $45252
R;Chlba, H.; Muramatuu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994
A;Title: Two human homologues of Saccharomyces cerevisiae SWIZ/SNF2 and Drosophila brahm
A;Reference number: $45251; MUID:94268902
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1647 <CHI>
A;Cross-references: GB:D26156; NID:g505087; PIDN:BAA05143.1; PID:g505088
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
F;1485-1540/Domain: bromodomain homology <BRO>
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Similarity 28.9%; Pred. No. 19;
37; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S45252
SNF2beta protein - human
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A;Cross-references: GB:Y00208; NID:951371; PIDN:CAA68364.1; PID:951372
A;Experimental source: strain Balb/c
A;Accession: A38763
A;Accession: A38763
A;Molecule type: mRNA
A;Residues: 1-270 < CODE2>
A;Cross-references: GB:Y00208; NID:951371; PIDN:CAA68364.1; PID:951372
A;Cene: Hox 1.3
A;Map position: 6
A;Introns: 187/3
A;Mtrons: 187/3
C;Superfamily: homeotic protein Hox A5; homeobox homology
C;Superfamily: homeobox; nucleus; phosphoprotein; transcription regulation
F;196-252/Domain: homeobox homology < HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 YSQPATSTHSPPDDPLPCSAVAPSPGSDSHHGGKNSLGNSSGASANAGSTHISSREGVGT 145
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Best Local Similarity 25.8%; Pred. No. 4.6;
Matches 55; Conservative 13; Mismatches 63; Indels 82; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 QEQPTSS-----72
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                                                    October 9, 2001, 15:58:35; Search time 15.11 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                         93435 seqs, 34255486 residues
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                                                                                                                                                                                                                                                                                                                                                                                  CCAA_HUMAN
CCYAA_NEDCR
CCAB_HUMAN
CMGA_BOVIN
HLES_DROME
SNZ4_HUWAN
HXA5_HUWAN
IE18_PRVIF
SG113_MOUSE
SG13_MOUSE
HXA5_HUMAN
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ZYX_CHICK
HERG_HUMAN
NKCR_MOUSE
ARVC_HUMAN
CCT_DROME
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LFY_ARATH
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Y553_HUMAN
Z174_HUMAN
IE63_MCMVS
NKC1_SQUAC
SPS2_CRAPL
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GAT3_HUMAN
VE2_HPV25
PAXI_CHICK
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAK4_HUMAN
                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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Match Length DB
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Q01513 podospora a	P35246 bos taurus	P20393 homo sapien	O15117 homo sapien	Q9y6j0 homo sapien	P20659 drosophila	P08462 rattus norv	P01211 bos taurus	P98193 rattus norv	P51514 rattus norv	Q63003 rattus norv
CYAA_PODAN	PSPD_BOVIN	NRD1_HUMAN	FYB_HUMAN	CABI_HUMAN	TRX_DROME	GRPB_RAT	PENK_BOVIN	DMP1_RAT	HTF4_RAT	SE5_RAT
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6.6	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8	8.8
80	79.5	79.5	79.5	79.5	79.5	79	79	79	79	79
35	36	37	38	39	40	41	42	43	44	4 5

## ALIGNMENTS

D O O O O O O O O O O O O O O O O O O O	RESULT 1  BAD_HURAN  CONSTRUCT 2  BAD_HURAN  STANDARD; PRI; 168 AA.  DE BAD_HURAN  CONSTRUCT 2  TO 1-NOV-1997 (Rel. 35, Created)  DE BAD GROBE CONTROL 35, Created)  DE BAD OR BEGG OR BCL218.  CONTROL 35, Created)  DE BAD OR BEGG OR BCL218.  CONTROL 35, Created)  CONTROL 35, Created)  DE BAD OR BEGG OR BCL218.  CONTROL 35, Created)  CONTROL 36, CALL 36, Last annotation update)  CONTROL 36, CALL 36, CALL 36, CALL 37, CALL 36, CALL 37,
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-oCT-2000 (Rel. 40, Last annotation update)
vOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL,
000555; Q92690; Q16290; Q99790; Q99791; Q99792; Q99793; P78510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=97141920; PubMed=8988170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1693-1807 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2038-2258 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurosci. 15:274-283(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genet. 15:62-69(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87:543-552(1996).
                                                                                                                                                                               NCBI_TaxID=9606
                                                                                                        (BI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                         Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.; "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
                                                                                                                                                                                                                                                                                                                                                                   61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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             121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                             121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22080 MW; 6C2BA910205053F7 CRC64;
                                                                                                                                             01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last Sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
                                                                                                                   204 AA
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                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                            TISSUE=Brain, and Thymus;
MEDLINE=95136361; PubMed=7834748;
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                                                                                                                     STANDARD;
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182
204 AA;
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Matches 126; Conserv
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
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CCAA_HUMAN I
ID CCAA_HUMAN
                                                                                                                   BAD_MOUSE
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                                                                                                    BAD MOUSE
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TISSUE-Cerebellum:
MEDLINE-97053792; PubMed-8898206;
Ophoff R.A., Terwindt G:M., Vergouwe M.N., van Eijk R., Oefner P.J.,
Hoffman S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E.,
Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
Ferrari M.D., Frants R.R.;
Familial hemiplegic migraine and episodic ataxia type-2 are caused by
mutations in the Ca2+ channel gene CACNLIA4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of cDNA clones containing CCA trinucleotide repeats
"Characterization of cDNA clones containing CCA trinucleotide repeats
derived from human brain."; 279-284(1955).

Somat. Cell Mol. Genet. 21:279-284(1955).

ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
IN A VARIETY OF CALCIUM DEPENDENT PROCESSES, INCLIDING MUSCLE
CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA IA
GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM
CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND
ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-
IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO
DUHYPROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-
                                                                                                                                                                                                                                                                                                                                                   TISSUE-Neuron;
MEDILTNE-99128614; PubMed-10049321;
MEDILTNE-991286614; PubMed-10049321;
Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
Harpold M.M., Johnson E.C., Williams M.E.;
"Structural elements in domain IV that influence biophysical and
pharmacological properties of human alphalA-containing
high-voltage-activated calcium channels.";
Biophys. J. 76:1384-1400(1999).
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MEDLINE-96102310; PubMed-8525433;
Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
McInnis M.G., Ross C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W., Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.; Attosomal dominant cereballar ataxia (SCA6) associated with small polyglutamine expansions in the alpha IA-voltage-dependent calcium channel."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95123449; PubMed-7823133; Barry E.L.R., Viglione M.P., Kim V.I., Froehner S.C.; Expression and antibody inhibition of P-type calcium channels in human small-cell lung carcinoma cells.";
                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVIA).
SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2)
                                                                         Homo sapiens (Human).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
CACNAIA OR CACNLIA4 OR CACH4 OR CACN3.
```

PRINTS; PR00167; CACHANNEL

IN A 1:1:1: RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE POREFORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE ACTIVITY SUBUNITS BETA AND ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
SUBCELLULAR LCCATION: INTEGRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; BI-1/1A-2, BI-1(V1),
GGCAG AND BI-1(V2,V3); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: BRAIN-SPECIFIC, MAINLY FOUND IN CEREBELLUM,
CEREBRAL CORPEX, THALAMUS AND HYPOTHALAMUS. NO EXPRESSION IN
PREDOMINANTY P-TYPE VSCC, THE Q-TYPE BEING A PROMINENT CALCIUM COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS

CURRENT IN CEREBELLAR GRANULE CELLS.
DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
PURDROPHORISIC TRANSMEMBRANE SEGMENT (S1, S2, S3, S5, S6) AND ONE
POSTITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A

SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
10 LYMORPHISM: THE POLY-GLN REGION OF CACMAIA IS POLYMORPHIC: 6 TO
17 REPEATS IN THE NORMAL POPULATION, EXPANDED TO ABOUT 21 TO 30
REPEATS IN SPINOCERREBELAR ATAXIA 6 (SCA6) PATIENTS. THERE SEEMS
TO BE A CORRELATION BETWEEN THE REPEAT NUMBER AND EARLIER ONSET OF THE DISORDER

DISEASE: EXPANSION OF A CAG REPEAT IN THE CODING REGION OF CACNAIA IS THE CAUSE OF ONE FORM OF SPINOCEREBELLAR ATAXIA 6 (SCA6), AN AUTOSOMIAL DOMINNAT DISORDER CHARACTERIZED BY SLOWLY PROGRESSIVE CEREBELLA ATAXIA OF THE LIMBS AND GAIT, DYSARTHRIA, NYSTAGWUS, AND MILD VIBRATORY AND PROPRIOCEPTIVE SENSORY LOSS. THESE SYMPTOMS ARE PROBABLY EXPLAINED BY SEVERE LOSS OF CEREBELLAR PURKINJE

MIGRAINE (FHM), ALSO KNOWN AS MIGRAINE FAMILIAL HEMIPLEGIC I
(MHP1), EPISODIC ATAXIA TYPE 2 (EA-2), ACETAZOLAMIDE-RESPONSIVE
HEREDITARY PAROXYSMAL CEREBELLAR ATAXIA (APCA), AND POSSIBLY OTHER
COMMUN TYPES OF MIGRAINES, FHM, A RARE AUTOSOMAL DOMINANT SUBTYPE
OF MIGRAINE WITH AURA, IS ASSOCIATED WITH ICTAL HEMIPARESIS AND,
IN SOME FAMILIES, PROGRESSIVE CEREBELLAR ATROPHY. EA-2 IS ANOTHER
AUTOSOMAL DOMINANT PAROXYSMAL CEREBELLAR ATROPHY. EA-2 IS ANOTHER
AUTOSOMAL DOMINANT PAROXYSMAL CEREBELLAR ATAXIA AND
MIGRAINE-LIKE SYMPTOMS, INTERICTAL NYSTAGMUS, AND CEREBELLAR DISEASE: DEFECTS IN CACNALA ARE THE CAUSE OF FAMILIAL HEMIPLEGIC

SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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ALT\_INIT. ALT\_INIT. ALT\_INIT. -; NOT\_ANNOTATED\_CDS 280115; -; NOT\_ANNOTATED\_CDS. U79666; AAB64179.1; -. U79663; AAB49674.1; ALT\_INIT. ALT\_INIT EMBL; AF004884; AAB61613.1; -. EMBL; AF004883; AAB61612.1; -. U79668; AAB49678.1; S76537; AAB33068.1; U06702; -; NOT\_ANNOT X99897; CAA68172.1; U79664; AAB49675.1; U79665; AAB49676.1; AAB49677.1; EMBL; Z80115; U79667 EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; 

-; NOT\_ANNOTATED\_CDS

InterPro; IPR002077; -. Pfam; PF00520; ion\_trans; 4.

InterPro; IPR000636; -. InterPro; IPR002077; -.

183086;

601011;

EMBL;

Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism; Disease mutation; Triplet repeat expansion. Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; CYTOPLASMIC (POTENTIAL).
31 OF REPEAT III (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
S2 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT III (POTENTIAL).
S3 OF REPEAT III (POTENTIAL). CYTOPLASMIC (POTENTIAL).
33 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
54 OF REPEAT II (POTENTIAL).
55 OF REPEAT II (POTENTIAL).
55 OF REPEAT II (POTENTIAL).
55 OF REPEAT II (POTENTIAL). SS OF REPEAT III (POTENTIAL). S6 OF REPEAT III (POTENTIAL). CYTOPLASMIC (POTENTIAL). SI OF REPEAT IV (POTENTIAL). S4 OF REPEAT III (POTENTIAL) S3 OF REPEAT IV (POTENTIAL). S2 OF REPEAT IV (POTENTIAL). CYTOPLASMIC (POTENTIAL). EXTRACELLULAR (POTENTIAL). S4 OF REPEAT IV (POTENTIAL). CYTOPLASMIC (POTENTIAL). S1 OF REPEAT II (POTENTIAL) EXTRACELLULAR (POTENTIAL). S2 OF REPEAT II (POTENTIAL) S6 OF REPEAT II (POTENTIAL) CYTOPLASMIC (POTENTIAL). S3 OF REPEAT I (POTENTIAL). EXTRACELLULAR (POTENTIAL). S4 OF REPEAT I (POTENTIAL). CYTOPLASMIC (POTENTIAL). S5 OF REPEAT I (POTENTIAL). (POTENTIAL) EXTRACELLULAR (POTENTIAL) S6 OF REPEAT I (POTENTIAL EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL) S2 OF REPEAT I 1358 1484 DOMAIN TRANSMEM **PRANSMEM** PRANSMEM PRANSMEM **PRANSMEM** PRANSMEM PRANSMEM **TRANSMEM** TRANSMEM DOMAIN REPEAT 

2313 POOOOOOOOOOOAVARPGRAATSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPG 2372 2373 PARSESPRACRHGGARWPASGPHVSEGPPGPRHHG------YYRGSDYDEADG 2419 ---PSPFR-----GRS----RSAPPNLWAAQRYGRELRRMXDEFV 122 Gaps 42 -----GLLWDAS--HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE---80; DB 1; Length 2505; 5 PEFEPSEQED-----SSSAERGLGPSP---AGDGPSGSGKHHRQAP : Pred. No. 6.9; 22; Mismatches 54; Indels Score 96; 10.6%; 23.5%; 48; Conservative Similarity Query Match Best Local Matches 43 82 Q ô á

11;

2477 PA--HGLARPRGPGSRKGLHEPYS 2498 DSFKKGLPRPKSAGTATQMRQSSS 146

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Similarity
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Q00975;
                                                                Query Match
Best Local Si
Matches 50)
              SEQUENCE
DOMAIN
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                                                                                                                                                                                                                                                                                                                             Kore-Eda S., Murayama T., Uno I.;
"Isolation and characterization of the adenylate cyclase structural
                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
ADENYLATE CYCLASE (EC. 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                                                                                                                                                                                          gene of Neurospora crassa.";
Jpn. J. Genet. 66:317-334(1991).
-!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE. -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY. -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR). -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucine-rich repeat; cAMP synthesis; Magnesium.
                                                                                                                                                                                                      Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
                                                               2300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; ...
InterPro; IPR001932; ...
Pfam; PF00509; LRR; 13.
Pfam; PF00481; PP2C; 1.
PRINTS; PR00019; LEURICHRPT.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
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CATALYTIC.
POLY-SER.
                                                                                                                                                                                                                                      Sordariales; Sordariaceae; Neurospora
                                                                PRT;
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MEDLINE=92000795; PubMed=1680356;
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                                                               STANDARD;
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986
1008
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                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
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                                                                                                                                                                                        CR-1 OR NAC.
                                                           CYAA_NEUCR
Q01631;
                                                                                                                                                                      CYCLASE)
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                                              CYAA_NEUCR
                                RESULT
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REPUBLICE OF 1-94 FROM N.A.

REQUENCE OF 1-94 FROM N.A.

RISSUE-Lung fibroblast;

RL SIDMITTED CALCIUM CHANNELS (VSCC) MEDIATE THE TITSUE-LUNG (FEB-1997) to the EMBL/GenBank/DDBJ databases.

CLOMITTED CALCIUM LONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DYISION ORELD EARTH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRANTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED.

CONTRACTIONS.N-GYTA (OMEGA-CTX-GYIA) AND BY OMEGA-AGATOXIN-ING CONTRACTION CHANNELS CONTRANNING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIHYDROPYRDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-VIA).

CC CALCIUM CHANNELS CONTRANNING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.

CC COMPLEASE, CONSISTING OF ALLHA-1, ALPHA-2, BETA AND DELTA SUBUNITS OF LINA ALL SUBUNIT IN MANY CASES, THIS SUBUNIT IS SUFFICIENT THE CHANNEL ACTIVITY. THE PORE-CONTRAND AND SUBUNITY IS SUBUNITY. THE AUXILLARY SUBUNITY BETA AND ALPHA-2/DELFA CHANNEL ACTIVITY. THE AUXILLARY SUBUNITY BETA AND ALPHA-2/DELFA CHANNEL ACTIVITY. THE AUXILLARY SUBUNITY BETA AND ALPHA-2/DELFA ALLIAND AND AND ALPHA-2/DELFA AND
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
III) (BIII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIRSRHSS------YPA-----GTEDDEGMGEEP-----SPFRGR---SRSA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 GGRDRDASPVPSRPRTPVPAPEVVPFLYQEADDIARYGEAPVRTSLTGFDRDRYIDSSQN 459
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                17 SAERGLGPSPAGDGPSGSGKHHR----QAPGLLWDASHQQEQPTSSSHH-----GGAGAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 PPKTSSSARSGHSIVHLPGHHKHNKSNEDPRALKPSLSREDSAASFARDFRNGSSSMMGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      63;
                                                                                                                                                                                             Length 2300;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).
                                               254752 MW; 52E79B90E6B17A7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPNLWAAQRYGREL-----RRMXDEFVDSFKKGLPRPKSAGT---
                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2339 AA
                                                                                                                                                                                        10.0%; Score 90.5; D 23.7%; Pred. No. 17; ive 23; Mismatches
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POLY-GLN.
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MEDLINE=92335886; PubMed=1321501;
                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
221
                                    2300 AA;
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- ALTERRATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1B-1 (SHOWN HERE) AND
ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE
CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.
-!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
PYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
PROBABLY REPRESENT THE VOLTAGE-SENORR NO ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
-!- PTH, PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002077; -.

InterPro; IPR002077; -.

Pfam; PF00520; Jon_trans; 4.

PRINTS; PR00167; CACHANNEL.

Ionic channel, Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.
                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SI OF REPEAT II (POTENTIAL).
S2 OF REPEAT II (POTENTIAL).
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S3 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT III (POTENTIAL).
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CYTOPLASMIC (POTEWITAL).
S3 OF REPEAT I (POTEWILAL).
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EMBL; M94173; AAA51898.1; -.
EMBL; U76666; AAC51138.1; -.
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REPEAT 82
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BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

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GSGSVNGSPLLSTSGASTPGRGGRRQLPOTPLTPRPSITYK
TANSSPIHFAGAQTSLPAFSFGRLSRGLSFHATLLQRDPLS QPLAPGSRIGSDPYLGQRLDSEASVHALPEDTLIFEEAVAT SGRSSRYSVYSSLTSGSPLARWONGYHCTLGLSSGGRAR HSYHHPDDJHWC -> AGSAVGFPHTTPCCRETPASASPWDL ALELALTLIWGSVWTVRPLSTPCLRTRSLSRRLWPPTRAAP CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY). CMGA\_BOVIN STANDARD; PRT; 449 AA.
P05059; P79392;
13-AUG-1987 (Rel. 05, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I)
(CONTAINS: VASOSTATIN-1; CHROMOSTATIN; CHROMACIN; PANCREASTATIN; WE14; CATESTATIN]. CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY 30; Gaps 8 EPSEQED----SSSAERGLGPSPA-----GDGPSGSGKHHRQAPGLLWDA------ 48 (BY SIMILARITY). PHOSPHORYLATION (BY CAPK) (POTENTIAL). 49 -SHQQEQPTSSSHHGGAGAV-EIRSRHSSYP-AGTEDDEGMGEEPS-PFRGRSRSAP 101 Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; PGLPTCPP (IN ISOFORM ALPHA-1B-2). 262494 MW; 17A45C6D1E76B39D CRC64; BINDING TO THE BETA SUBUNIT (BY S6 OF REPEAT III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT IV (POTENTIAL).
S3 OF REPEAT IV (POTENTIAL).
S3 OF REPEAT IV (POTENTIAL).
S4 OF REPEAT IV (POTENTIAL).
S4 OF REPEAT IV (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL). 10.0%; Score 90; DB 1; Length 2339; 30.8%; Pred. No. 18; 16; Mismatches 35; Indels CYTOPLASMIC (POTENTIAL). (POTENTIAL) SIMILARITY POLY - SER Ouery Match
Best Local Similarity 30.8%
Warches 36; Conservative 1719 1748 256 1563 1675 2339 1365 1655 458 314 663 2339 AA; 1709 2050 2118 379 1365 1655 256 1563 1675 2164 1553 1564 1583 1602 1622 663 451 DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM MOD\_RES CA\_BIND CARBOHYD CARBOHYD CARBOHYD VARSPLIC SEQUENCE FRANSMEM TRANSMEM PRANSMEM NP\_BIND DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN CMGA\_BOVIN CHGA. SITE SITE SITE SITE 셤 ò ò 셤

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Bovidae; Bovinae; Bos

NCBI\_TaxID=9913;

SEQUENCE FROM N.A.

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MEDILNE-66311345; PubMed=3018587; Iacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.; Iacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.; "Bovine chromogranin A sequence and distribution of its messenger RNA in endocrine tissues."; Nature 323:82-86(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Ca2(+)-induced conformational change and aggregation of chromogranin
                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M. van Dorsselbarc A., Aunis D., Metz-Boutigue M.-H.; "Antibacterial activity of glycosylated and phosphorylated chromogranin A-derived peptide 173-194 from bovine adrenal medullary
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"Identification of the secretory vesicle membrane binding region of
chromogranin A.";
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"Chromostatin, a 20-amino acid peptide derived from chromogranin A,
                                                                                                                                            Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J., Mallet J., Huttner W.B.;
"The primary structure of bovine chromogranin A: a representative a class of acidic secretory proteins common to a variety of peptidergic cells.";

EMBO J. 5:1495-1502(1986).
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                                      hormone
                 lacangelo A.L., Grimes M., Eiden L.E.;
"The bovine chromogramin A gene: structural basis for hormone
regulation and generation of biologically active peptides.";
Mol. Endocrinol. 5:1651-1660(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87260925; PubMed=3474638;
Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary structure of bovine pituitary secretory protein I (chromogranin A) deduced from the cDNA sequence."; Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibits chromaffin cell secretion.";
Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991)
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Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 19-45, AND CALCIUM-BINDING.
MEDLINE-90354431; PubMed-2387861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromaffin granules.";
J. Biol. Chem. 271:28533-28540(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Chromaffin granules;
MEDLINE=97067080; PubMed=8910482;
                                                                                                           SEQUENCE FROM N.A.
MEDLINE-86300648; PubMed=3755681;
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MEDLINE-97228583; PubMed-9074643;
MEDLINE=92140395; PubMed=1779968;
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CHARACTERIZATION OF CATESTATIN.

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                                                                  discrete
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FUNCTION: VASOSTATIN-1 HAS ANTHBACTERIAL ACTIVITY AGAINST GRAMPOSITIVE BACTERIA M.LUTEUS, B.SUBTILIS, S.PYROGENES, M.FORTUITUM, S.ANTRUS AND L.MONOCYTOGENES AND SAGINST GRAM-NEGATIVE BACTERIA E.CLLACARE, S.TYPHIMURIUM, K.PNEUMONIAE AND PAURUGINOSA.

POSSESSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.FUMIGATUS, A.BRASSICOLÀ, N.HEMATOCOCCA, F.CULMORUM AND F.OXYPORUM AND AGAINST S.CEREVIASE AND C.ALBICANS YEAST. INACTIVE AGAINST T.MENTAGROPHYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CABOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND. MEDLINE=9945928; PubMed=10527498; Bauer S.H., Zhang X.Y. van Dongen W., Claeys M., Przybylski M.; Chromogranin A from bovine adrenal medulla: molecular characterization of glycosylations, phosphorylations, and sequence heterogenelties by mass spectrometry."; haterogenelties by mass spectrometry."; Anal. Biochem. 274:69-80(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular modeling of the catestatin region reveals a beta-
strand/loop/beta-strand structure secured by hydrophobic interactions
and predictive of activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE FROM CHROMAFFIN CELLS.
                     Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H., Gill B.M., Parmer R.J.;
"Novel autocrine feedback control of catecholamine release. A discret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASS SPECTROMETRY: MM-8584.9; METHOD-MALDI; RANCE-19-94.
MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                               MEDLINE-99000113; PubMed-9786174;
Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
"Mechanism of cardiovascular actions of the chromogranin A fragment
catestatin in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20219105; PubMed-10753865;
Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
Aunis D., Metz-Boutigue M.-H.;
                                                                                chromogranin a fragment is a noncompetitive nicotinic cholinergic antagonist.";
                                                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELING OF CATESTATIN.
MEDLINE-99025567; PubMed-9809795;
Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
Khan I., Parmer R.J., O'Connor D.T.;
"Mechanism of action of chromogranin A on catecholamine release:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T.MENTAGROPHYTES.
SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Antibacterial and antifungal activities of vasostatin-1, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  terminal fragment of chromogranin A.";
J. Biol. Chem. 275:10745-10753(2000).
                                                                                                                                  Clin. Invest. 100:1623-1633(1997).
MEDLINE=97439785; PubMed=9294131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION OF VASOSTATIN-1.
                                                                                                                                                                               CHARACTERIZATION OF CATESTATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELEASE FROM THE PANCREAS
                                                                                                                                                                                                                                                                                                 Peptides 19:1241-1248(1998).
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EMBL; EMBL; EMBL;

PIR;

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                                                                                                        MEDLINE=93041287; PubMed=1419850; Maier D., Stumm G., Kuhn K., Preiss A.; Maier D., Stumm G., Kuhn K., Preiss A.; Maier D., Stumm G., Kuhn K., Preiss A.; Maier D. Stumm G., Kuhn K., Preiss A.; Maier Drosophila gene involved in neural development, encodes a novel, serine rich protein."; Mech. Dev. 38:143-156(1992).

-!- FONGTION: IS A POTENT ANTAGONIST OF NEUROGENIC GENE ACTIVITY DURING SENSORY ORGAN DEVELOPMENT. THE EXPRESSION OF DISTINCT CELL FATES BY THE TRICHOGEN (SHAFT) / TORMOGEN (SOCKET) SISTER CELL PAIR DEPENDS ON THE LEVEL OF H ACTIVITY: A CERTAIN THRESHOLD LEVEL OF H ACTIVITY IS REQUIRED, BELOW WHICH BOTH SISTER CELLS ADOPT THE TORMOGEN FATE.
Bang A.G., Posakony J.W.;
"The brosophila gene Hairless encodes a novel basic protein that
controls alternative cell fates in adult sensory organ development.";
Genes Dev. 6:1752-1769(1992).
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                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
TISSUE SPECIFICITY: OVARY, EMBRYOS, LARVAL AND PUPAL IMAGINAL
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W; A94BF1A27579E2F1 CRC64;
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AAVA -> RLLP (IN REF. 2).
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S -> A (IN REF. 2).
QH -> LL (IN REF. 2).
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THR-RICH.
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
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POLY-ALA.
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ALA-RICH.
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EMBL; X67239; CAA47664.1; -.
HSSP; P04002; 1WFA.
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P04002; 1WFA.
FlyBase; FBgn0001169; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al protein; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     946
974
1008
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703
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                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 KSAGTATQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              773 STSGSASQ 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   642
879
937
964
979
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702
891
964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SN24_HUMAN
P51532;
01-OCT-1996 (
01-OCT-1996 (
01-OCT-2000 (
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SEQUENCE
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SN24_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidas; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXD--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 EVEKSDEDSDGDRPQASPGLGPGP-----KVEEDNQAPG-----EEEEAPSNAH-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 -- PLASLPSPKYPGPQAKEDSEGPSQGPA-----SREKGLSAEQ--GRQTEREEEEEK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFEPSEQE---DSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Amidation; Glycoprotein; Calcium-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 87.5; DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism; 3D-structure; Antibiotic; Fungicide SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EFVDSFKKGLPR------PKSAGTATQMRQSSSW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 WEEAEAREKAVPEEESPPTAAFKPPPSLGNKETQRAAPGW 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOGRANIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 5.2;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1077 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PANCREASTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VASOSTATIN-1.
CHROMOSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATESTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHROMACIN
                       5/9258, AAB21297.1; JOINED.
5/9260; AAB21297.1; JOINED.
5/9262; AAB21297.1; JOINED.
5/9264; AAB21297.1; JOINED.
5/9266; AAB21297.1; JOINED.
5/9268; AAB21297.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE-92387549; Pubmed-1516831;
                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PRO0659; CHROMOGRANIN.
PROSITE; PSO0422; GRANINS_1; 1.
PROSITE; PSO0423; GRANINS_2; 1.
                                                                                                                                         X04012; CAA27636.1;
X04298; CAA27841.1; -.
M16971; AAA30765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 24.4%;
Conservative 1
                                                                                    EMBL; S79264; AAB21297.1;
EMBL; S79266; AAB21297.1;
EMBL; S79268; AAB21297.1;
EMBL; X04012; CAA27636.1;
                                                                                                                                                                                                                                                                              PDB; 1CFK; 22-MAR-99.
GlycoSuiteDB; P05059; -.
InterPro; IPR001819; -.
InterPro; IPR001990; -.
                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01271; Granin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                        PIR; A41520; A41520
                                                                                                                                                                                                                                                             PIR; A28033; A28033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAIRLESS PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterian J.E., McCready P.M., Skowronski E., Viswanathan V., Bangerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Brower A., Stilwagen S., Burkhart-Schultz K., Gordon L., Dias J., Brower A., Stilwagen S., Dan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Liu S., A banganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., A Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J., Darte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.; Carrano A.V.; Carrano A.V.; Carrano A.V.; Carrano A.V.; Carrano A.V.; Chee EMBL/GenBank/DDBJ databases.

-1- FINCTION: TRANSCRIPTIONAL COACTIVATOR COOPERATING WITH NUCLEAR HORMONE RECEPTORS TO POTENTIATE TRANSCRIPTIONAL ACTIVATION.

-1- SIMILARITY: CONTAINS 1 BROMODOMAIN.

-1- SIMILARITY: BELONGS TO THE SNR2/RADS4 HELICASE FAMILY.
                                                                                                                                                                                                                         Khavari P.A., Peterson C.L., Tamkun J.W., Mendel D.B., Crabtree G.R., "BRGI contains a conserved domain of the SWI2/SNF2 family necessary for normal mitotic growth and transcription."; Nature 366:170-174(1993).
                                                                                                                                                                                                                                                                                                                                                Khavari P.A., Peterson C.L., Tamkun J.W., Mendel D.B., Crabtree G.R., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiba H., Muramatsu M., Nomoto A., Kato H.;
"Two human homologues of Saccharomyces cerevisiae SWIZ/SNF2 and
Drosophila brahma are transcriptional coactivators cooperating with
the estrogen receptor and the retinoic acid receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001487; -.
InterPro; IPR001487; -.
InterPro; IPR001687; -.
InterPro; IPR001650; -.
Pfam; PF00176; SNP2_N; 1.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00501; helicase_C; 1.
PRINTS; PR00503; BROMODOMAIN_1; 1.
PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS0014; BROMODOMAIN_1; 1.
Transcription regulation; Nuclear protein; Activator; Bromodomain;
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA
                                                                                                     Euteleostomi;
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLU.
ATP (POTENTIAL).
DEGH BOX.
POLY-GLU.
BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 22:1815-1820(1994).
                                                           SMARCA4 OR SNF2L4 OR BRG1 OR SNF2B.
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94268902; PubMed=8208605;
                                                                                                                                                                                                    MEDLINE=94050144; PubMed=8232556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 814-1474 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U29175; AAB40977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC006127; AAC97987.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAA05143.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786
884
1364
1547
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                                                                                  Homo sapiens (Human)
                                          PROTEIN HOMOLOG 1).
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 603254; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: NUCLEAR.
-i- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
                                                                                                                           9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH---RQAP-GLLWDASHQQEQPTSSSHHGGA 64
                                                                                                                                                         30 PSPGPSPGSAHSMMGPSP---GPPSAG--HPIPTQGPGGYPQDNMHQMHKPMESMHEKGM 84
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Coding sequence and expression of the homeobox gene Hox 1.3.";
                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-89232713; PubMed=2565857;
Odenwald W.F., Garbern J., Arnheiter H., Tournier-Lasserve E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr. Taylor G.F., Palmer-Hill F.J., Friedrich V. Jr. Taylor G. A. P. Tani M., Lazzarini R.A.;
"Expression of a homeo domain protein in noncontact-inhibited cultured cells and postmitotic neurons.";
Genes Dev. 1:482-496(1987).
                                                                Length 1647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88328807; Pubmed-2901335;
Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labeit S.,
Lehrach H., Gruss P.;
                                                                                              Indels
1571 1584 POLY-GLU.
1647 AA; 184585 MW; 7B785E7953277FID CRC64;
                                                                                                                                                                                            65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQ 108
                                                                                                                                                                                                                          85 SDDPRYNQMKGMGMRSGGHAGMGPPPSPMDQHSQGYPSPLGGSE 128
                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HOMEDBOX PROTEIN HOX-A5 (HOX-1.3) (M2).
                                                                                                                                                                                                                                                                                                       270 AA
                                                                               Pred. No. 24;
9; Mismatches
                                                                Score 86.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88056292; Pubmed=2890554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE=96205869; Pubmed=8635464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 102:349-359(1988).
                                                                9.68;
                                                                             29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes Dev. 3:158-172(1989).
                                                                                               31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
DNA-BINDING SPECIFICITY.
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lazzarini R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoprotein
                                                                                                                                                                                                                                                                                                    HXA5_MOUSE
P09021;
              SEQUENCE
                                                                                                                                                                                                                                                                                       HXA5_MOUSE
                                                                                               Matches
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  11;
         (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                       73 ----HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDEFVDSFKKG 128
                                                                                                                                                                                                                                                                                         82; Gaps
                                                                                                                                                                                                                                                                                                          10 SEQ-EDSSSAERG-----LGPSPAGDGPSGSGKHHRQ-----APGLLWDASHQ 51
                                                                                                                                                                                                                                                                                                                              31 SEQFRDSASMHSGRYGYGYNGMDLSVGRSGSGHFGSGERARSYAAGASAAP----AEPR 85
                                                                                                                                                                                                                                                                                                                                                 52 QEQPTSS-----AGAVEIRSR---- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
                                                                                                                                             PRINTS: PR00024; HOMEOBOX.
PRINTS: PR00025; ANTENNAPEDIA.
PROSITE; PS00027; HOMEOBOX_1: 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS50071; HOMEOBOX_2: 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of bovine chromogranin B deduced from cDNA
                                                                                                                                                                                                                                                                   ; Score 86; DB 1; Length 270;
; Pred. No. 4;
13; Mismatches 63; Indels
Usage by
                                                                                                                                                                                                                                        DC4BDDA8FE62766E CRC64;
                                                                                                                                                                                                                    ANTP-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 AA
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                         192 GPEGKRARTAYTRYQTLELEKEFH--FNRYLTR 222
                                                                                                                                                                                                                                                                                                                                                                                                                              129 LPRPKSAGTATOMRQSSSWTRVFQSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.";
Biochim. Biophys. Acta 1089:124-126(1991)
         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Adrenal chromaffin;
MEDLINE-91223091; PubMed-2025642;
Bauer J.W., Fischer-Colbrie R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG1_BOVIN STANDARD; F P23389; 002707; 01-NOV-1991 (Rel. 20, Created)
                                    EMBL; M36604; AAA37838.1; -.
EMBL; Y00208; CAA68364.1; -.
EMBL; X16840; CAA34738.1; -.
EMBL; M28021; AAA37837.1; -.
PIR; SO7812; WJWS13.
HSSP; P02833; ISAN.
                                                                                                                                                                                                                                       270 AA; 29237 MW;
                                                                                                                                                                                                                                                                     9.5%;
                                                                                                                                      Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                         Transcription regulation.
                                                                                                                                                                                                                                                                                        55; Conservative
                                                                                                        MGD; MGI:96177; Hoxa5.
InterPro; IPR001356; -.
InterPro; IPR001827; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE; SECRETOLYTIN]
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                               TRANSFAC; T00377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                     176
                                                                                                                                                                                                                             DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                               Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Adrenal chromaffin;
MEDLINE-95262699; PubMed=7744058;
Strub J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
van Dorsselaer A., Aunis D., Metz-Boutique M.-H.;
Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolytin, the endogenous C-terminal fragment of residues 614-626 with antibacterial activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: O-GLYCOSYLATED (PROBABLE). SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                            of
                             foo S.H., Kang Y.K.;
"Identification of the secretory vesicle membrane binding region ihromogranin B.":
                                                                                                                                                       TISSUE-Adrenal medulla;
Grandy D. R., Leduc R., Makam H., Flanagan T., Diliberto B.J.,
Thomas G., Civelli O., Viveros O.H.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECRETOLYTIN.

BY SIMILARITY.

SULFATATION (POTENTIAL).

SULFATATION (BY SIMILARITY).

N -> 5 (IN REF. 1)

N -> D (IN REF. 2).

SEAPGL -> FRSPRAS (IN REF. 3).

T -> M (IN REF. 2).

T -> M (IN REF. 2).

P -> R (IN REF. 2).

P -> R (IN REF. 2).

P -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfatation; Cleavage on pair of basic residues; Signal. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECRETOGRANIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAWK PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X55027; CAA38846.1; --
EMBL, U88551; AAC48720.1; --
EMBL, X55489; CAA39109.1; --
EMBL, X55489; CAA39109.1; --
ELS ST5901; S15901 --
InterPro; IPR001819; --
Ffam; PF01271; Granin; I-
PROMITE; PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS_1; 1.
TISSUE-Adrenal medulla;
MEDLINE-97282588; PubMed-9136897;
                                                                              chromogranin B.";
FEBS Lett. 406:259-262(1997).
                                                                                                                                    SEQUENCE OF 21-646 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         646
6484
6484
57
158
315
64
70
70
70
181
181
181
481
                                                                                                                                                                                                                                                           SEQUENCE OF 634-646.
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634
36
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70
93
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261
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MOD_RES
CONFLICT
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PEPTIDE
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                                         YOO S.H.
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09-580523-la.rsp

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[2]
REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR MATRIX AND IN DENTINOCENESIS.
--- TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH
PARTICUARLY IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESSED
IN LIVER AND SKIN.
                                                                                                                   246 PGESEEDA-----SPEVDKRHSRPRHHGRSRP----DRSSQEGNPPLEEESHVGTG 293
                                                                                                                                           65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGR------ELRRMX 118
                                                                                                                                                          J. Dent. Res. 76:754-760(1997).
                                                                      Gaps
                                                                                           9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH--RQAPGLLWDASHQQEQP--TSSSHHGGA. 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.;
"Cloning and expression analysis of the bovine dentin matrix acidic
phosphoprotein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELTIN MATERIX ACIDIC PHOSPHOPROTEIN 1.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
9BFA9A74F6450865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                     24;
                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1 PRECURSOR (DENTIN MATRIX
                                             DB 1; Length 646;
                                                                     Indels
M -> V (IN REF. 2).
420DB1178FD9E415 CRC64;
                                                                    53;
                                            Query Match 9.5%; Score 86; DB 1
Best Local Similarity 27.9%; Pred. No. 9.8;
Matches 36; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                           510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Tooth;
MEDLINE=97263952; PubMed=9109824;
        73339 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U47636; AAB09412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366
55491
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
510
351
370
427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                       taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                               PROTEIN-1) (DMP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364
510 AA;
         646 AA;
                                                                                                                                                                                                        :| :: |
352 EESLEQENK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                          DEFVDSFKK 127
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                          DMP1_BOVIN
Q95120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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CONFLICT
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                                                                                                                                                                                                                                                   RESULT 11
DMP1_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 ASHQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEEPSPFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 RSPVSSNPNSSSSSTTTVAVEPVAR-----GPEKDEDGLGLAGDGGAPLQRQPRRRRAG 344
51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------APGLLWD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheung A.K.;
Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELLICHAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF PHOSPHORYLATION.
                                     ||:: | | | | | | | | : | |: | || 347 PSQENSSESQEEALHES-RGDNPDNATSHSRE------HQADSESSEEDVLDKPSDS
                                                                                                                                                                            397 ESTSTEEQADSESHE-----SLRSSEES-PESTEEQNSSSQEGAQTQSRSQESP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheung A.K.; "DNA nucleotide sequence analysis of the immediate-early gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

DOMAIN 390 405 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1461;
                                                                                                                               ----QEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 PNLWAAQRYGRELRRMXDEFVDS-----FKKGLPRPKSAGTATQMRQSSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7F31E7ABE403B208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71;
PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PSEQEDSSSAERGLGP--SPAGDG-PSGS---GKHHRQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
RMMEDIATE-EARLY PROTEIN IE180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.5%; Score 85.5; D
28.8%; Pred. No. 25;
iive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 17:4637-4646(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89315207; PubMed-2546124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last seq
01-FEB-1994 (Rel. 28, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X15120; CAA33214.1; -.
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Best Local Similarity 28.88
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudorabies virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31523;
                                                                                                                                                                                                                                                                                          RESULT 12
IE18_PRVIF
ID IE18_PRVIF
AC P11675;
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8

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Gaps

39;

9.5%; Score 85.5; DB 1; Length 510; 25.2%; Pred. No. 8.4; tive 12; Mismatches 35; Indels 3

Conservative

Query Match Best Local'Similarity Matches 29; Conserv

11

g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 TSTHSPQPDPLPCSAVAPSPGSDTHHGGKNSLSNSSGASADAGSTHISSREGVGTASGAE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS. ALSO BIRDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF: 5'-CYNATTA[FG]7-3'. SUBCELLULAR LOCATION: NUCLEAR. DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
                                                                                                                                       Lazzarini R.A.; ^{\prime\prime} Remarkable intron and exon sequence conservation in human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ-EDSSSAERG-----LGPSPAGDGPSGSGKHHRQ--APGLLWDASHQOEQPT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 SEQFRDSASMHSGRYGYGYNGMDLSVGRSGSGHFGSGERARSYAASASAAPAEPRYSQPA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS-----AGAVEIRSRHS-SYPAGTE 81
                                                                                                                                                                                                                                                                                                                                                                                                                              Genome 31:745-756(1989).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART
                                                                                                                  Tournier-Lasserve E., Odenwald W.F., Garbern J., Trojanowski J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 195-260 FROM N.A. MEDLINE=90215256; PubMed=2576652; MEDLINE=90215256; PubMed=2576652; Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R., Gaudino G., Stornaiuolo A., Caffero M., Faiella A., Simeone A.; "Organization of human class I homeobox genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%; Score 84; DB 1; Length 270;
44.5%; Pred. No. 5.7;
ve 17; Mismatches 78; Indels
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                Bradshaw H., Hinds K., Keppler D.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> S (IN REF. 2).
6583BF22562BC9AC CRC64;
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                                                                                                                                                                              homeobox Hox 1.3 genes.";
Mol. Cell. Biol. 9:2273-2278(1989).
                                                                         ŠEČUENCE FROM N.A.
MEDLINE-89313782; PubMed-2568583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00025; ANTENNAPEDIA.
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29359 MW;
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nes 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, A32799; WJHUIC.
HSSP; P02833; 1SAN.
TRANSFAC; T01702; -.
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270 AA;
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CONFLICT
SEQUENCE
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                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RETINOIC ACID-INDUCIBLE E3 PROTEIN (HEMATOPOIETIC-SPECIFIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96437028; PubMed=8839844;
Scott L.M., Mueller L., Collins S.J.;
"E3, a hematopoietic-specific transcript directly regulated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P20715; 043367;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HOMEOBOX PROTEIN HOX-A5 (HOX-1C).
HOMOS Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retinoic acid receptor alpha.";
Blood 88:2517-2530(1966).
-- TISSUE SPECIFICITY: PRESENT IN THE MYELOID, B-LYMPHOID,
ERYTHROID LIMBAGES, ABSENT IN NONHEMATOPOIETIC CELLS.
               E---GALRRGRGFSSSSGGSDSDLSPARSPSAPRAPAAAAARRSASS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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647CCB5FDA7BC73E CRC64
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                                                                                                                    215 AA
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Pred. No. 4.1;
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                                                                                                                  PRT;
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                                                                                                                    STANDARD;
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30-MAY-2000 (
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Matches 33;
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                                                                                                                    ST13 MOUSE
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                                                                                            ST13_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 151-160; 235-244 AND 267-282, AND PHOSPHORYLATION SITES. SEQUENCE OF 151-160; 235-244 AND 267-282, AND PHOSPHORYLATION SITES. MEDLINB-94237860; PubMed-8182057;
Butt E., Abel K., Krieger M., Palm D., Hoppe V., Hoppe J., Walter U.; "CAMP- and CGMP-dependent protein kinase phosphorylation sites of the focal adhesion vasodilator-stimulated phosphoprotein (VASP) in vitro and in intact human platelets.";
J. Biol. Chem. 269:14509-14517(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cioning of the VASP (vasodilator-stimulated phosphoprotein) genes in human and mouse: structure, sequence, and chromosomal localization."; Genomics 36:227-233(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: FOCAL ADHESIONS.
PTM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT
PROTEIN KINASE (CGPK) IN PLATELETS.
DDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQM 141
                                 151 EDAPASSEQASAQSEPSPAPPAQPQIYPWMRKLHISHDNI-----GGPEGKRARTAYTR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIANGE 19755215; PubMed=7737110;
Reinhard M., Giehl K., Abel K., Haffner C., Jarchau T., Hoppe V., Jockus B.M., Walter U.;
Jockus B.M., Walter U.;
Jockus Profiline U.;
Ingand for profilins ";
EMBO J. 14:1583-1589(1995)

-! FUNCTION: ACTIN ADD PROFILIN-BINDING MICROFILAMENT-ASSOCIATED PROTEIN. MAY ACT IN CONCERT WITH PROFILIN TO CONVEY SIGNAL TRANSDUCTION TO ACTIN FILAMENT PRODUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning, structural analysis and functional expression of
the proline-rich focal adhesion and microfilament-associated protein
VASP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmer M., Fink T., Fischer L., Hauser W., Scherer K., Lichter P.,
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-95129547; PubMed-7828592;
Haffner C., Jarchau T., Reinhard M., Hoppe J., Lohmann S.M.,
                                                                                                                                                                                                             P50552; 093035;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-CCT-2000 (Rel. 40, Last annotation update)
VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).
                                                                                                                                                                                              380 AA.
                                                                                                                                                                                                PRT;
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MEDLINE-96411679; PubMed-8812448;
                                                                     RQSSSWTRVFQSWWDRNLGR 161
                                                                                          205 YQTLELEKEFH--FNRYLTR 222
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                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                        sapiens (Human).
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                                                                                                                                                                                              VASP_HUMAN
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EMBL; Z46389; CAA86523.1; -. EMBL; X98534; CAA67147.2; -.

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252 KAESGRSGGGLMEEMNAMLARRRKATOVGEKTPKDESANOEEPEARVPAOSESVRRPWE 311
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                            17 SAERGLG-----PSPAGDGPSGSGKHHRQAPGL------LWDASHQQEQ---PTS- 57
                                                                                                                      POLY-GIX.
POLY-GIX.
POLY-SER.
PHOSPHORYLATION (BY CAPK AND CGPK).
PHOSPHORYLATION (BY CAPK AND CGPK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 GRSRSAP-----PNLWAAQRYGRELRRMXDEFVDSFKKGLPRPK 133
                                                                                                                                                                                                                                                                                                  9.3%; Score 84; DB 1; Length 380; 24.9%; Pred. No. 8.1; Live 18; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ---SSHHGGAGAVE----IRSRHSSYPAG---TEDDEGMGEEPS-----
                                                                                                                  POLY-PRO.
EMBL; X98533; CAA67147.2; JOINED. MIM; 601703; -.
                                   InterPro, IPR001960, -.
Pfam; PF00568; WH1; 1.
Phosphorylation; Actin-binding.
                                                                                                                                                                                                                                             39830 MW;
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                                                                                                                 186
222
222
362
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157
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278
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Matches 43; Conserv
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Output) Output Sequential Mono Sequential Mono

Oguha8 homo sapien Oguq35 homo sapien Ogva18 drosophila

Minimum DB : Maximum DB :

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Result

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Searched:

O9eru8 mus musculu O9va96 drosophila

008719 rattus norv mus musculu oryza sativ

P70429 Q91wj9

homo sapien homo sapien caenorhabdi

09nte2 09ne12 09ns89

homo sapien

homo sapien homo sapien

Q9ntp8 h Q9ulk9 h Q15206 h Q05331 h

OM protein

Run on:

Sequence:

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Ottille S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G., Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.; J. Biol. Chem. 0:0-0(1997).
EMBL; AF021792; AAB72092.1; -.
EMBL; AF031523; AAB8124.1; -.
SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.9%; Score 901; DB 4; Length 168; ilarity 99.4%; Pred. No. 2.2e-76; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97083574; PubMed=8929532;
MANGH H.G., Rapp U.R., Reed J.C.;
"Bcl.-2 targets the protein kinase Raf-1 to mitochondria.";
Cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                             168 AA
                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequenc)
01-MOV-1998 (TrEMBLrel. 08, Last annotal
BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).
                         Q9NEL2
Q9NTP8
Q9ULK9
Q15206
Q05331
Q9ERU8
Q9VA96
O08719
                                                                                                                09UPX1
098321
09NAN8
095884
09UC2
09UC2
09TG4
09TG4
09UQ36
09UQ4
09UQ36
                                                                                                       Q9LWJ9
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         09NS89
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1082
2472
6220
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Matches 167; Conserv
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Query Match
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09jhx1 rattus norv
09d5k9 herpesvirus
09df20 brachydanio
09ns37 homo sapien
09tv26 oryza saiv
095387 homo sapien
095387 homo sapien
09688 homo sapien
09kn4 leishmania
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09upq9 homo sapien
009000 mus musculu
09h8q9 trypanosoma
036421 alcelaphine
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632.714 Million cell updates/sec
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070256 rattus norv
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1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                          425026 seqs, 132305027 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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070256
0914X1
0919N2
0905K9
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09KN37
09FVZ6
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Gapop 10.0 , Gapext 0.5
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Q919N2 PRELLMINARY; PRT; Q919N2; 01-0CT-2000 (TrEMBLrel. 15, Created)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                   Best Local Similarity 74.69
Matches 126; Conservative
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Best Local Similarity
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MEDLINE-98194755; PubMed=9535132;
D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
"Caoning and expression of the programmed cell death regulator Bad in the rat brain.",
Neurosci. Lett. 243:137-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hsu S.Y., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptosis in mammalian cells by 14·3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1848-1867(1997).
EMBL; AR003523; AAC53374-11; -
SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 HHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXD 119
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-OCT-2000 (TremBirel. 15, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE
                 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
10-NOV-1998 (TrEMBLrel. 08, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 70.1%; Score 632.5; DB 11; Best Local Similarity 74.6%; Pred. No. 2.3e-51; Matches 126; Conservative 11; Mismatches 25;
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BAD OR BAD-ALPHA.
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SEQUENCE FROM N.A.
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SEQUENCE THOM N.A.
Functional characterization of two splice variants of rat bad and their interaction with bcl.w in sympathetic neurons.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF03127; AAC15100.1: --
EMBL, AF279910; AAF91427.1: --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 MFQIPEFEPSEQEDASTTDRGLGPSLTEDQP---GPY--LAPGLLGSIVQQQPGQAANNS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                70.1%; Score 632.5; DB 11; Length 205; 74.6%; Pred. No. 2.3e-51; Live 11; Mismatches 25; Indels 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 EFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                    205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
BAD-BETA.
BAD-BETA.
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391 EKEKSFMADNGMGPSRGGKPFGRGGRRRGPTLASGTNSEASNASE--TESDH----- 442
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                                                                                                                                                                                                                                    MEDLINE=20501265; PubMed=11046149;
Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;
"Characterization of dFMR1, a Drosophila melanogaster Homolog of the Fragile X Mental Retardation Protein.";
Mol. Cell. Biol. 20:8536-8547(2000).
EMBL; AF305882; AAG22046.1; --
SEQUENCE 569 AA; 63906 MW; 2E66A0689F7EDFB5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lu R., Misra V.; "Zhangfei: a second cellular protein interacts with herpes simplex virus accessory factor HCF in a manner similar to Luman and VP16."; Nucleic Acids Res. 28:2446-2454(2000).
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
KH DOMAIN CONTAINING RNA-BINDING PROTEIN FWRI.
Brachydanio rerio (Zebrafish) (Zebra danio).
Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Actinopterygii; Neopterygii: Teleostei: Euteleostei: Ostariophysi: Oypriniformes: Cyprinidae: Rasborinae: Danio.
NCBL_TAXID=7955;
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 569;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.
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InterPro; IPRO01871; --
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BRLZ; 1.
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Mammalia, Eutheria, Primates,
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 AA; 28859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.29
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.9
Best Local Similarity 32.3
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZF.
Homo sapiens (Human)
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NS37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 DEGMGEEP----SPFRGRSRSAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
Hayward G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  502 PRTERRRGSAQRGHPPPGAGQRPSGPTGGHPAAPGAPGPRSPRTERRRGSAQRGHPPPGA 561
                                                                                                                                                                                                                                  MEDLINE-20373792; PubMed-10917738;
Inohara N., Nunez G.;
"Genes with Homology to Mammalian Apoptosis Regulators Identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG----GA 64
                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 203.5; DB 13; Length 95; 48.9%; Pred. No. 7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100; DB 14; Length 608; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-----QRPSGPTGGHPAAPGAPGPPNPERGSGPADPP---AATRLPLEPR 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF200364; AAF23950.1; -- SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    77F5CDE879E69FF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 TOMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROMSOSPSWLAFL - - WSHKESDAESRPAE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BABOON LYMPHOCRYPTOVIRUS BA65;
                                                                                                                                                                                                                                                                                                Zebrafish.";
Cell Death Differ 7:509-510(2000).
EMBL: AF231017; AAF6662.1; ...
NON TER SEQUENCE 95 AA: 10804 MW; 77F5CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%;
            01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Matches 37; Conserv
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                         BAD (FRAGMENT).
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RESULT

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Q9DF20 Q9DF20;

RESULT Q9DF20 ID Q91 AC Q91

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STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Budal J., Zismann V., Pal G., Bowman C.L., Fujil C.Y., Vankken S.E.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBb0073N24 genomic sequence.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC078840; AAA13631.1; -.
SEQUENCE 867 AA; 94083 MW; 4FEA69EIBFCOCB2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     :: ::| || || || :|| 330 KEEAAAARGGGDDPLSHSHLGGGGGTGKEAAAAPTPTRGASRGGGGGADADAGSEQEDAA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 -----QPISSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         809 TSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPGPARSESPRACRHGGARWPASG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GLLWDAS- 49
                                                                                                                                                                                                                                                                                                                                                                                                             ---GLLWDASHQOE--- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 -HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEE------PSPFR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Black J.L., Snutch T.P., Lennon V.A.;

Partial sequence of Homo sapiens P/Q-type voltage-gated calcium channel alpha I (alpha IA) subunit isolated from small cell lung carcinoma cell line, SCC 9, cDNA library.";

SMDMITTED (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF100774; AAC77460.1;

InterPro; IPR000636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                      Length 867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1999 (TrEMBLE-1. 10, Last sequence update)
01-JUN-2000 (TrEMBLE-1. 14, Last annotation update)
VOLTAGE-DEPENDENT P/Q TYPE CALCIUM CHANNEL ALPHA 1A
                                                                                                                                                                                                                                                                                                                         10.7%; Score 96.5; DB 10; 28.7%; Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                   44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 95.5; DI
Pred. No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          13 EDSSSAERGLGPSPAG----DGPSGSGKHHRQAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SSSAERGLGPSP---AGDGPSGSGKHHRQAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             980 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002111; -. Pfam; PF00520; ion_trans; 1. PRINTS; PR00167; CACHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.6%;
ilarity 25.1%;
Conservative 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 790 AWGGGPDPLSHSHLGGGG---
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 28.7
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| | | |
836 RREERRLGR 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR00207
                                                               SEQUENCE FROM N.A.
                      NCBI_TaxID=4530;
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL136518; CAB66246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 -HSSYPAGTEDDEGMGEEPSPFRGRSRSAP--PNLWAAQRYGRELRRMXDEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AETLFAERAEGYDHAGHEGA--HGETGKGPPLPGLDAPARQGSPL------PGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG--GAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE REPLICATION PROTEIN.
01-yza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                          Streptomyces coelicolor.,
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; .
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Brown S.P., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUCATE PEOCESSI, HHH; 1.
SMART; SM00278; HHH; 1.
DNA-Binding.
SEQUENCE 355 AA; 36853 MW; ElE9DOA574CCABDE CRC64;
                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.9%; Score 98; DB 2; Best Local Similarity 28.5%; Pred. No. 0.17; Matches 43; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                867 AA.
                                                                                                                             355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 PRPKSAGTATOMROSSSWTRVFQSWWDRNLG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 DAPTGPGTAWRERAGSALRERMPLWLQTRCG 136
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
194 GLARLLSRLSGVGLRLTTSLFR 215
                                                                                                                                                                                                                                   PUTATIVE DNA-BINDING PROTEIN.
                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                         SCC123.06C
                                                                                                                                               Q9RDL8;
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983 AGATGLOL-----PGVTVDD----SDPDPOTOLKRGNIPNDFLROMFYTLGDYRDICI 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRY------ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI 69
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                                        Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95330812; PubMed=7541722;
Baruch D.I., Pealosoke B.L., Singh H.B., Bi X., Ma X.C., Feldman M., Taraschi T.F., Howard R.J., "Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and adherence receptor on the surface of parasitized human cell 82:77-87(1995).
EMBL, 027393; AAA89134.1; -.

NON_TER 1729 1729 AA: 195156 MW; 7BFEEC2131FFBA11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     802 AEQRITUTDDR----SPSAGGPASADVEHRSA-----SQPQQPHS---HAGGSAI-V
                                                                                                                                                       STRAIN-FRIEDLIN;
Whyler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock Nayler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock Nayler P.J., Suskin S., Stuart K.D.;
Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005941; AAF34290.1;
InterPro; IPR00194; TROPOMYOSIN.
SEQUENCE 923 AA; 103964 MW; C229C15F6448F7C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 1729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                         45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O25734 PRELIMINARY; PRT; 1729 AA. Q25734; O1-NOV-1996 (TIEMBLIEL. 01, Created) O1-NOV-1996 (TIEMBLIEL. 01, Last sequence update) PI-NOV-1998 (TIEMBLIEL. 08, Last annotation update) PFEMPI VARIANT 2 OF STRAIN MC (FRAGMENT).
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :99
                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                             10.5%; Score 94.5; DB 26.4%; Pred. No. 0.93; tive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.5%; Score 94.5; D
Best Local Similarity 21.6%; Pred. No. 1.8;
Matches 42; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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GPPQP 901
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Q25734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2335 TSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPGPARSESPRACRHGGARWPASG 2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-20219126; PubMed-10753886; MEDINE-20219126; PubMed-10753886; Medine-20219126; PubMed-10753886; Medine-2019126; PubMed-10751848 K., Saegusa H., Fujigasaki H., Toru S., Marakoshi T., Ishikawa K., Saegusa H., Tanabe T.; Spinocerebilar ataxia type 6 mutation alters P-type calcium channel function."; Isloi. Chem. 275:10893-10898(2000). EMBL; AB035727; BAA94766.2; -.
                869 PHVSEGPPGPRHHG------YYRGSDYDEADGPGSGGGEEAMAGAYDAPPPVR 915
                                                      -----GRS----RSAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQ 143
                                                                                -----GRS----RSAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
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                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ALPHAIA-VOLTAGE-DEPENDENT CALCIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
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                                                                                                                                                                                                                                                                               PRT; 2506 AA
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18; Mismatches
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PR00167; CACHANNEL.
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O9NKN4;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 25.19
Matches 46; Conservative
                                                                                                                                                                                                                                                                               PRELIMINARY;
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TISSUE-CEREBELLUM:
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                                                                                                                                    144 SSS 146
                                                                                                                                                                            971 PYS 973
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               1032 GGDRDIVGDTIVSITEGESTKKKISKIIEGFLK-----KQTVTSPSPRDTSSRTPVHPQT 1086
111 -----GRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVF--- 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Indels 49; Gaps
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                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                   Query Match 10.4%; Score 93.5; DB 4; Length 549; Best Local Similarity 25.0%; Pred. No. 0.68; Matches 41; Conservative 17; Mismatches 57; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| | | | : :
-----NSMPR-----LPTDLDVEGPWFRHYDFRQSCWVRAISQ 485
                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 62.2 KDA PROTEIN.
DKF2P434P2235.
                                                                                                                                                    549 AA.
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                                                                              1087 SVEKTPOOTWWEAN 1100
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Q9H0B9
ID Q9H0B9
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Murine BCL-XL/BCL-
Murine BAD protein
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305.943 Million cell updates/sec
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Mutant BCL-XL/BCL-
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1 MFQIPEFEPSEQEDSSSAER.....RVFQSWWDRNLGRGSSAPSQ 168
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                          October 9, 2001, 15:57:35
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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## ALIGNMENTS

Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad; Human Bcl-xL/Bcl-2 associated death promoting polypeptide. AAW55779 standard; Protein; 168 AA programmed cell death; apoptosis 96US-0717123. 97WO-US16991. (first entry) Horne WA, Oltersdorf T; (IDUN-) IDUN PHARM INC. WPI; 1998-217267/19. N-PSDB; AAV25877. Homo sapiens. WO9812328-A2 18-SEP-1997; 20-SEP-1996; 17-JUL-1998 26-MAR-1998 AAW55779; AAW55779 RESULT 

Claim 8; Fig 1; 41pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cell proliferation; APOP-1; cancer; inflammation; infection; trauma; neurodegenerative disease, ischaemic injury; wasting disease.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                untarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as cancers, e.g. lymphoma and hormone dependent tumours, autoimmune diseases, e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis and viral infections, e.g. herpesvirus, povvirus or adenovirus infection. Bad can also be used for detection and diamnosis
            The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-Xl results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be
                                                                                                                                                                                                                                                                                                                                                                           99.9%; Score 901; DB 19; Length 168; 99.4%; Pred. No. 3.4e-87; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell proliferation protein APOP-1.
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                                                                                                                                                                                                                                                                                            detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                          168 AA;
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The present sequence is the human APOP-1 protein. This protein, which shares structural and chemical homology with Bcl-2, is involved in cell proliferation. Its coding sequence was isolated by screening a synovial tissue cDNA library using a computer search for amino acid sequence alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated inflammation such as Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, athersociencesis, Crohn's disease, ulcerative colitis, diabetes mellitus, emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myosthenia gravis, myocardial or pericardial inflammation, osteoporosis, rheumatoid cartinis, syndrome and autoimmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulation, infections, crauma, disorders with associated apoptosis including AIDS and other infectious and genetic immunodeficiencies, meurodegenerative diseases such as Alzheimer's diseases and parkinson's disease, ischeemic injuries such as Marcheimer's diseases and parkinson's diseases including cachexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autolmmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 hggagaveirsrhssypagteddegmgeepspfrgrsrsappnlwaagrygrelrrmsde 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.9%; Score 901; DB 21; Length 168; 99.4%; Pred. No. 3.4e-87; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BAD mutant amino acid sequence SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APOP-) APOPTOSIS TECHNOLOGY INC
Example 8; Fig 1; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.4
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         168 AA;
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WPI; 2001-138734/14.

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The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

Bel-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

fragment, which contains amino acid substitutions at Seril8 of a human

BAD, Seri55 of a murine BAD (longer murine BAD) or Seril3 of a murine

BAD, Seri55 of a mutine BAD (longer murine BAD) or Seril3 of a murine

BAD, seri55 of a mutine BAD. (1) has immonstablant, antiviral,

notropic, antilschaemic, vulnerary, cytostatic, antiviral,

antiarthritic, antilnflammatory and immunosuppressive activities, and

can be used as an apoptosis inducer or inhibitior. BAD polypeptides and

polynucleotides can be used for screening candidate compounds and drugs

for activity that promote cell survival or apoptosis. Other uses include

indentified and (mutant) BAD polypeptides are useful in treating

immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

death, reperfusion cell death, wound healing, cancer, viral infections,

lymphoproliferative conditions, arthritis, infertility, inflammation and

autoimmune diseases. The present sequence represents a specifically

claimed human BAD mutant amino acid sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic.
                                    New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 3.4e-87;
0; Mismatches 1;
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                                                                                                                                     Claim 1; Page 147; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 AA;
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05-JUN-2000; 2000WO-US15449.

14-DEC-2000

(UYYA ) UNIV YALE.

04-JUN-1999;

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The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKPI, SKP2), SKP2-like proteins (ET) and CUL-1 (a member of the cullin, CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                     Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                       Claim 5; Page 102-103; 162pp; English.
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                           Kondo T;
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                           Tsvetkov LM,
                                                                                        WPI; 2001-061703/07.
N-PSDB; AAC84599.
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                           Zhang H,
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XX X X D D X X D D D X X D D X X D D X X D D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X
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RESULT
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                            The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with BG1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; vulnerary; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infection; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                  54 QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
                                                                                                                                                                                                                                                                                        52 qptssshhggagaveirsrhssypagteddegmgeepspfrgararpppnlwaagrygre 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                      1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPG-----LLWDASHQQE
                                                                                                                                                                                                                                 114 LRRMXDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ
                                                                                                                                                                         Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                               Indels
                                                                                                                                                                      Score 747; DB 18;
Pred. No. 5.4e-71;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 148-149; 157pp; English.
            Claim 1; Column 11-12; 7pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                            AAB70370 standard; protein; 162
                                                                                                                                                                         82.8%;
83.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-138734/14.
                                                                                                                                                                                     Similarity
                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200110888-A1.
                                                                                                                                                                         Query Match
Best Local Simil
Matches 146; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apoptosis,
Serli3 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB70370;
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The present invention describes an isolated or synthetic polypeptide

(1) Comprising a less than full length amino acid sequence of a mutant
Bel-XL/Bel-2 associated cell death requiator polypeptide (BAD) or its
fragment, which contains amino acid substitutions at Serl18 of a human
BAD, Serl55 of a murine BAD (longer murine BAD) or Serl13 of a murine
BAD (shorter murine BAD) (1) has immunostimulant, neuroprotective,
nootropic, antiischaemic, vulnerary, cytostatic, antiviral,
antiarthritic, antiinflammatory and immunosuppressive activities, and
can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
polynucleotides can be used for screening candidate compounds and drugs
for activity that promote cell survival or apoptosis. Other uses include
inducing or inhibiting apoptosis in a cell. Candidate compounds
identified and (mutant) BAD polypeptides are useful in treating
immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
death, reperfusion cell death, wound healing, cancer, viral infections,
lymphoproliferative conditions, arthritis, infertility, inflammation and
autoimmune diseases. The present sequence represents a specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mfqipefepseqedasatdrglgpsltedqp---gpy--lapgllgsnihqqgraatnsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
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hte= "BH1 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "BH2 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bcl-x(L)/bcl-2 associated death promoter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.5%; Score 645; DB 22; 75.0%; Pred. No. 2.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-1997
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Tue Oct

96US-0733505

18-OCT-1996;

(UNIW ) UNIV WASHINGTON.

Korsmeyer SJ;

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This sequence represents the murine bcl-x(L)/bcl-2 associated death promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with brownoter (Bad) gene. Bad is a 22.1 kD protein which interacts with col-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-2. Bad expression can accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell ine expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be conserved by the contact of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter-useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.5%; Score 645; DB 17; Length 204; 75.0%; Pred. No. 3.8e-60; Live 12; Mismatches 24; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine BCL-XL/BCL-2 associated cell death regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. AIDS, senescence or ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61315 standard; Protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 1; 130pp; English.
                      94US-0333565
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                                                                                                                                                                              WPI; 1996-251465/25.
N-PSDB; AAT29479.
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                                                                                                                            Korsmeyer SJ
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Best Local Si
Matches 126;
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fragments of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

Cor prevent diseases associated with reduced apoptosis, e.g. cancer, inflammation and autoimmune disease. Polynuclectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as ABDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family corrections in the cytosol, thus promoting cell survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3; serine phosphorylation; post-translational modification; apoptosis; signal transduction regulator; phosphoserine phosphatase; senescence; immunodeficiency disease, neurodegenerative disease; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.5%; Score 645; DB 19; Length 204; 75.0%; Pred. No. 3.8e-60; ive 12; Mismatches 24; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                                                   Claim 1; Fig 10; 95pp; English.
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Best Local Similarity 75.09
Matches 126; Conservative
                                                                                                                              WPI; 1998-261422/23.
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09-580523-la.rag

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immunosuppressive; apoptosis inducer; apoptosis inhibitor;
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AAW61317
ID AAW613
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                                                                                                                                                                                                                                                                                                                                to the 14-3.3 protein which is a signal transduction regulator.
Modulators of phosphorylated BAD, which act through inhibition/activation
of a phosphoserine phosphatase, are useful for preventing/treating
increased/decreased apoptosis in a cell. The increased apoptosis may
result from immunodeficiency diseases, senescence, neurodegenerative
disease, ischaemic cell death, reperfusion cell death, infertility and
wound-healing. Decreased apoptosis may result from cancer, viral
infection, lymphoproliferative conditions, arthritis, infertility,
phosphorylated compared to unphosphorylated BAD polypeptide and/or total
BAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
                                                                                                                                                                                                                                                                                               This sequence represents a novel serine-phosphorylated protein, BAD (Bcl-XI/Bcl-2 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine-phosphorylated Bcl-X-l/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
viral infection; lymphoproliferative condition; arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
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75.0%; Pred. No. 3.8e-60;
ive 12; Mismatches 24;
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            inflammation; autoimmune diseases
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                                                                                                         97WO-US15871.
                                                                                                                               96US-0707868.
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Best Local Similarity
Matches 126; Conserv
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(1) comprising a less than full length amino acid sequence of a mutant fragment, which contains amino acid sequence of a mutant Bal, Seri55 of a mutane Bab (longer mutine Bab) or Seri18 of a mutane Bab, Seri55 of a mutane Bab (longer mutine Bab) or Seri18 of a mutane Bab, Seri55 of a mutane Bab. (I) has immunostimulant, neuroprotective, notropic, antischaemic, vulnerary, cytostatic, antiviral, antistratic, antilifiammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. Bab polyapetides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds inducting or inhibiting apoptosis in a cell. Candidate compounds inducting or inhibiting apoptosis in a cell. Candidate compounds inducting or inhibiting apoptosis in a cell. Candidate compounds immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically calamed longer murine Bab mutant amino acid sequence from the present
Immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated or synthetic polypeptide
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; Pred. No. 3.8e-60;
12; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APOP-) APOPTOSIS TECHNOLOGY INC.
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75.0%;
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                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                    15-FEB-2001
                                                                                                                                                                                            Synthetic.
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AAW61317;

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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat corprevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infinamation and autoimmune disease. Polynuclectide sequences encoding inflammation and autoimmune disease. Polynuclectide sequences encoding cransgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as Albs, neurodegeneration, editor and an association and monthibitors are an individual and monthibitors.
                                                                                 Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                         Mutant BCL-XL/BCL-2 associated cell death regulator #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 60; 95pp; English.
                                                                                                                                                                                                                                                                                                 97WO-US19175.
                                                                                                                                                                                                                                                                                                                                         18-OCT-1996; ' 96US-0733505.
(first éntry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               Korsmeyer SJ;
07-0CT-1998
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Gaps 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQOEQPTSSSH 60 ; 9 70.8%; Score 639; DB 19; Length 204; 73.8%; Pred. No. 1.6e-59; ive 14; Mismatches 24; Indels 6 Best Local Similarity 73.8 Matches 124; Conservative Query Match ò HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

3;

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at cosition 112 and/or 136, relative to the murine BAD 204 as sequence. The presents sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery Wutant BAD proteins are used to treat concreases intracellular delivery Wutant BAD proteins are used to treat concrease infection, lymphoproliferation, arthritis, infertility.

Con prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

Con prevent diseases. Polynuclectide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is cetermined by measuring relative amounts of phosphorylated and non-phosphorylated baD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not ceterminelies with BCL-2 or RCL-XL but instead binds to 14-3-3 family contents in the cytosol, thus promoting cell survival. The mutants with Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection. New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection Mutant BCL-XL/BCL-2 associated cell death regulator #1. Ā AAW61316 standard; Protein; 204 Claim 7; Page 59; 95pp; English. 96US-0733505. (first entry) (UNIW ) UNIV WASHINGTON. WPI; 1998-261422/23. 204 AA; N-PSDB; AAV27834 Korsmeyer SJ; WO9817682-A1 18-OCT-1996; 07-0CT-1998 30-APR-1998 Mus sp. Synthetic. AAW61316; Sequence RESULT 12 AAW61316 g 

204 AA;

Sequence

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death regulator) proteins, having a maino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The presents equence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility.

Inflammation and autoimmune disease. Polynucleotide sequences encoding transgenic animals for use as disease models or in drug screening. BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serie-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-XL/BCL-2 associated cell death regulator; BAD protein;
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HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                      121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                  Mutant BCL-XL/BCL-2 associated cell death regulator #3.
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                                                                                                                                                                                                                                                                                   AAW61318 standard; Protein; 204 AA.
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N-PSDB; AAV27836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                    61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                                                                                                                                                     Gaps
                                                                  1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH
                                                                                    New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
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 Length 204;
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                                 24;
 DB 19;
               1.6e-59;
                   Pred. No. 1.6e
14; Mismatches
 Score 639;
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70.8%;
73.8%;
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                                 Matches 124; Conservative
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                   Similarity
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determined by measuring relative amounts of phosphorylated and non-

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phosphorylated man, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                                                                      Sequence
888888888
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59 AA;

Gaps ; 0 Length 59; Indels Score 310; DB 19; Pred. No. 1.5e-25; 0; Mismatches 1; 34.48; 98.38; Query Match 34.4 Best Local Similarity 98.3 Matches 58; Conservative

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63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDEF 121 

## RESULT 15

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AAW61320 standard; Protein; 59 AA AAW61320

AAW61320;

07-OCT-1998 (first entry)

Mutant BCL-XL/BCL-2 associated cell death regulator #5.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

Mus sp. Synthetic.

WO9817682-A1

30-APR-1998

97WO-US19175. 17-OCT-1997;

96US-0733505 18-OCT-1996;

(UNIW ) UNIV WASHINGTON

Korsmeyer SJ;

WPI; 1998-261422/23. N-PSDB; AAV27838.

New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection

Claim 8; Page 73; 95pp; English.

death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is present invention describes mutant BAD (BCL-XL/BCL-2 associated cell The 1 

determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus romoting cell survival. The mutants with Ser substituted cannot bind 14-3-3. 88888888

59 AA; Sequence

Gaps ó Length 59; 1; Indels Score 310; DB 19; Pred. No. 1.5e-25; Mismatches ; 0 34.4%; 98.3%; 58; Conservative Similarity Query Match Best Local S Matches

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63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDEF 121 δ g

Search completed: October 9, 2001, 15:59:14

Job time: 99 sec

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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-452-007-2
US-08-455-543A-47
US-08-223-305C-47
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                                                                                                                                                                                                                                                                197339 seqs, 20590346 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDER ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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99.4%; Pred. No. 3.7e-86;
.ive 0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,123

FILING DATE: 20-SEP-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 9-ID 1929

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9049

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
                        US-09-227-420-3
US-09-227-420-3
US-09-227-420-1
US-08-6131-470-17
US-09-026-587-4
US-09-026-587-4
US-09-226-470-4
US-09-226-012-2
US-09-226-012-2
US-09-228-65-2
US-08-922-865-2
US-08-922-865-2
US-08-933-565-26
US-08-933-565-26
US-08-931-955-26
US-08-931-955-26
US-08-931-955-26
US-08-659-214A-16
US-08-659-214A-16
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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08-08-717-123-2
5 Sequence 2, Application US/08717123
7 Patent No. 5965703
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393
393
393
318
318
380
11159
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1478
424
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121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                                                                                                   ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                              Gainesville
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Best Local Similarity
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                                                                                                                                                                                                                                                                              CITY: Gainesvi
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                       ADDRESSEE:
                                                         RESULT 3
US-08-665-617-2
                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 146;
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US-08-985-335-7
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
                    61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
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                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
UNDHAR OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY, AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0421 US
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 901; DB 3;
Pred. No. 3.7e-86;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                  ...ureSSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto STATE: CA CUNTRY: USA 2.70.
                                                                                                                                                                                                                Sequence 1, Application US/08985335 Patent No. 6080847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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MEDIUM TYPE: Diskett
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TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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LIBRARY: SINC.
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                                                                                                                                                                             RESULT 2
US-08-985-335-1
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US-08-985-335-1
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54 QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPG-----LLWDASHQQE 53
                                             GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 LRRMXDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 747; DB 1;
Pred. No. 3.3e-70;
                                                                                                                                                                       E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROLIFERATION
Sequence 2, Application US/08665617
Patent No. 5663316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08985335 Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Colley, Neil C.
TITLE OF INVENTION: PROTEINS AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-800
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
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83.4%;
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAORYGRELRRMXDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 71.5%; Score 645; DB 1; Length 204; Best Local Similarity 75.0%; Pred. No. 1.6e-59; Matches 126; Conservative 12; Mismatches 24; Indels
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of mouse BAD."
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Patent No. 5834209
GERERAL INFORMATION:
APPLICAT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl.x/Bcl.2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                OPERATION SYSTEM: TO LOUS, MS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-0CT-1994
CLASSIFICATION: 435
ATTONENTYAGENT INFORMATION:
NAME: SMITH, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET UNMBER: 15726A-000700
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-2402
TELEPHONE: (415) 326-242
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 anino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US 08/333,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein FEATURE:
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COTHER INFORMATION:
COTHER INFORMATION:
CS-333-565-2
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CITY: Palo Alto
STATE: California
COUNTRY: US
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Pred. No. 1.8e-69;
0; Mismatches 26; Indels
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Patent No. 5622852
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: BC1-x/BC1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATORNEY-AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 95,749
REGISTRATION NUMBER: PF-0421 US
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.5
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650-622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: GenBank
CLONE: 1683637
                                                                                       Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                   USA
                                                                                                                                                      94304
                                                                                    CITY: Pa.
STATE: CA.
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US-08-333-565-2
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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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                                                                                                                                                                                                       71.5%; Score 645; DB 2; Length 204; 75.0%; Pred. No. 1.6e-59; Live 12; Mismatches 24; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: P-ID
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 535-9001
TELEFRAX: (619) 535-904
INFORMATION FOR SEO ID NO: 3:
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COUNTRY: United States
                                                                                                                                                                                                                                                  Conservative
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Matches 126; Conservative
           SEQUENCE CHARACTERISTICS
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                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
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Best Local Similarity
Matches 126; Conserv
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                                                   TYPE: amino STRANDEDNESS:
                                                                                                                                        US-08-733-505A-1
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US-08-717-123-3
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERRAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 204;
                                                                                                                                                                                                                                                                                                                                                                                               /note= "Deduced amino acid sequence
of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.5%; Score 645; DB 2; Best Local Similarity 75.0%; Pred. No. 1.6e-59; Matches 126; Conservative 12; Mismatches 24
                                                                                              15726A-000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/733,505
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
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ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REPERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITh, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: 0.
US-08-661-479-2
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COMPUTER READABLE FORM:
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STATE: MISSOURI
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMERNS, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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APPLICATION NUMBER: US/08/733,505A
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                                                                                                                        NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
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AER: 965458
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.29
Best Local Similarity 74.49
Matches 125; Conservative
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MOLECULE TYPE: peptide
US-08-733-505A-13
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COMPUTER READABLE FORM:
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CLASSIFICATION: 530
                                                                                                                                                                                                    STREET: 7733 FORG
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
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MISSOURI
                          GENERAL INFORMATION:
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STATE:
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                                                   61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDE 120
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                                                                             98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMTDE 157
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43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: RORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.2%; Score 642; DB 2; Best Local Similarity 74.4%; Pred. No. 3.3e-59; Matches 125; Conservative 13; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL, & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
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US-08-733-505A-13
; Sequence 13, Application US/08733505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-518
TELEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63105
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Length 204;

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TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: ESEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MISSICOUNTRY: USZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                    US-08-733-505A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-733-505A-56
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US-08-733-505A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 HGGAGAMETRSRHSAYPAGTEEDEGMEEELSPFRGRSRAAPPNLWAAQRYGRELRRMSDE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-733-505A-55
Sequence 55, Application US/08733505A
Sequence 55, Application US/08733505A
Sequence 55, Application US/08733505A
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

70.8%; Score 639; DB 2;
Best Local Similarity 73.8%; Pred. No. 6.8e-59;
Matches 124; Conservative 14; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REERRANCE/OCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 204 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-733-505A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 7733 FOI CITY: ST. LOUIS STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDEF 121
                                                                                                                                                                                                                                                        1 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDEF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION:
BL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 PCRSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                   Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 59;
                                                                                                                                              Score 310; DB 2; Length 59
Pred. No. 1.7e-25;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 307; DB 2;
Pred. No. 3.5e-25;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/POCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
                                                                                                                                                   34.48;
98.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.0%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 96.69
                                                                                                                                            Query Match 34.4'
Best Local Similarity 98.3'
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-733-505A-56
                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMXDEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-733-505A-58

Sequence 58, Application US/08733505A

Sequence 58, Application US/08733505A

Sequence 58, Application US/08733505A

Sequence 58, Application US/08733505A

GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: G.
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400

CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.0%; Score 307; DB 2; Length 59; Best Local Similarity 96.6%; Pred. No. 3.5e-25; Matches 57; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/73,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPRAX: (314) 727-5188
TELECOMMUNICATION INFORMATION:
TELEPRAX: (314) 727-5188
TELEPRAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 57:
SPOURMET SEQUENCE CHRARCTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
                                                                                                                                                                                                         ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI COUNTRY: USA
Sequence 57, Application US/08733505A Patent No. 5856445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-733-505A-57
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Search completed: October 9, 2001, 15:58:34 Job time: 59 sec

09-580523-1b.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2001, 15:58:09; Search time 24.69 Seconds Run on:

(without alignments)
518.320 Million cell updates/sec

09-580523-1B 905 1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168 Perfect score: Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bad protein - mous	erythrocyte membra	probable immediate	hypothetical prote	RNB6 protein - rat	N-type calcium cha	profilaggrin - hum	omega-conotoxin-se	hypothetical prote	chromogranin A pre		hypothetical prote	chromogranin B pre	polycomb protein e	serine-rich protei	2beta protein –	hypothetical prote	LFY floral meriste	hypothetical prote	probable potassium		pHL ElFl - human	hypothetical prote	probable transcrip	hypothetical prote	filaggrin precurso	vasodilator-stimul	hypothetical prote	in - chicken
	Des	bad	ery	pro	hyp	RN	N-t	pro	ome	hyp	chr	eye	hyp	chr	pol	ser	SNF	hyp	LFY	hyp	pro	hon	pHI	hyp	pro	hyp	£i]	vas	hyp	zyxin
SUMMARIES		A55671	T18396	T03166	T42702	JC5614	T45115	A35938	A42566	T30757	A41520	T13049	T43500	S15901	T13154	A44067	845252	T05221	B38104	T02858	I38465	WJMS13	154810	T00037	T51947	T29146	A28444	S51797	ഹ	4358
	A :	A5	T1	$_{ m T0}$	Τ4	β	Τ4	A3	A4	Т3	A4	11	$\mathbf{T4}$	S	11	A4	S4	T0	B3	T <sub>0</sub>	13	N	15	O.L	T5	T2	A2	S2	S	A4
	DB							7			7	7	•	7	7	7	7	7	7	7	7			7					~	7
	Query Match Length	204	1729	1300	834	393	2237	2248	2339	336	449	2715	222	646	2023	1077	1647	343	420	751	1159	270	134	1323	1392	1562	313	380	381	542
dр	Query	71.4	10.4	10.3	10.2	10.0	6.6	6.6	6.6	•	9.8	9.8	٠.	•	9.6	٠		٠	٠	4.	9.4	4.6	9.3	9.3				٠	6.9	9.3
	Score	646	94.5	93	92	90.5	90	90	90	89.5	88.5	88.5	88	87	87	86.5	86.5	86	86	85.5	85.5	82	84.5	84.5	84.5	84.5	84	84	84	84
	Result No.	п	7	m	4	5	9	7	8	6	10	11	12	13	14	15	16	17	. 18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	profilaggrin - rat	enkephalin e-12 pr	homeotic protein H	filaggrin - mouse	probable secretory	heterogeneous ribo	Balbiani ring 2.1	subtilisin-type al	cyclin T - fruit f	bumetanide-sensiti	myosin-IA - Acanth	microtubule-associ	endozepine related	LFY floral meriste
S07132	T24786	A34615	EQBOA	WJHU1C	A31488	T36677	A33616	A45294	н83736	T13033	A53491	T32734	A54602	T49431	A38104
~	7	~		-	7	~	~	7	~	7	7	~	~	~	7
988	380	625	263	270	254	523	558	749	792	1097	1191	1215	1734	337	424
9.3	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1
84 9.3	83.5 9.2		83 9.2	83 9.2						82.5 9.1		82.5 9.1		82 9.1	82 9.1

## ALIGNMENTS

A55671 bad protein - mouse

C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C;Accession: A55671
R;Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Reference number: A55671; MUID:95136361
A;Ccession: A55671
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: MRNA
A;Residues: 1-204 <ANA
A;Residues: 1-204 <ANA
A;Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C;Keywords: heterodimer

3; Gaps . 9 Length 204; Query Match 71.4%; Score 646; DB 2; Length 20 Best Local Similarity 75.0%; Pred. No. 3.1e-45; Matches 126; Conservative 13; Mismatches 23; Indels

61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120 q ò

98 HGGAGAMETRSRHSSYPACTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 157 q

121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168 δ

158 q

erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fr C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: 15-oct-1999 #sequence\_revision 15-oct-1999 #text\_change 09-Jun-2000 C;Accession: T18396 R;Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bl, X.; Ma, X.C.; Feldman, M.; Taraschi, Cell 82, 77-87, 1995 A;Title: Cloning the P. falciparum gene encoding PfEMPI, a malarial variant antigen a A;Reference number: 218925; MUID:95330812 A;Accession: T18396 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1729 CBAR> A;Centeics: 1-1729 CBAR> A;Centeics: EMBL:U27339; NID:9914920; PID:9914921; PIDN:AAA89134.1

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C; Accession: JC5614
R; Ohta, S.; Mineta, T.; Kimoto, M.; Tabuchi, K.
Biochem. Biophys. Res. Commun. 237, 307-312, 1997
A; Title: Differential display cloning of a novel rat cDNA (RNB6) that shows high expr
A; Reference number: JC5614; MUID: 97415794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: This protein belongs to Ena/VASP family member, and is involved in the dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human C;Species: Homo sapiens (man) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNB6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSR----HSSYPAGTEDDE-GMGEEPSP----FRGRSRSAPP-----NLWAAQRY--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-393 <OHT>
A;Cross-references: GB:U70211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HSSYPAGTEDDEGMGEEP--SPFRG-RSRSAPPNLWAAQRYGRELRRMAD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GRELRRMADEFVDSFKK-----GLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 EDSSSAERGLGPSP---AGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                             64;
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                                                                                                                                                                                                                                                                                                                               Indels
                    A; Accession: T46502
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 213-834 <AA2>
A; Cross-references: EMBL:AL137336
A; Experimental source: adult testis; clone DKFZp434B239
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 90.5; Di
28.2%; Pred. No. 3.5;
iive 16; Mismatches
                                                                                                                                                                                                                                                                                                                             18; Mismatches
                                                                                                                                                                                                                                                                           Score 92;
Pred. No. 6
                                                                                                                                                                                                A; Note: DKFZp434F117.1; DKFZp434B239.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 EFVDSFKKGLPRPKSAGTATOM 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPVSSL---LSRVKPAGSVNDV 350
                                                                                                                                                                                                                                                                      10.2%;
27.1%;
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.1%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
A; Reference number: Z23029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: JC5614
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 G 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
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T45115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable immediate early protein - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C;Accession: T03166
R;Ensser, A; Pflanz, R: Fleckenstein, B.
J. Virol. 11, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: 214840; MUID: 97404659
A;Accession: T03166
A;Accession: T03166
A;Accession: T03166
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1300 < cms>
A;Residues: 1-1300 < cms>
A;Cross-references: EMBL:AF005370; NID: q2333967; PIDN: AAC58118.1; PID: q23338034
C;Superfamily: collagen alpha 2(1) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein DKFZp434F117.1 - human (fragment)
N;Alternate names: hypothetical protein DKFZp434B239.1
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C;Accession: T42702; T46502
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A;Reference number: 22234
A;Accession: T42702
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-834 <AAA>
A;Cross references: EMBL;Ali33028
A;Experimental source: adult testis; clone DKFZp434F117
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
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                                                                                                                                                                                                                                                                                                                                                                                                           1032 GGDRDIVGDTIVSITEGESTKKKISKIIEGFLK-----KQTVTSPSPRDTSSRTPVHPQT 1086
                                                                                                                                                                                                                                                                                                        926 PSGNESSPSEKLPQGPTPETTKETPESSLLHAFVSPPRLRRFLPW---HKFKEQWKAQHG 982
                                                                                                                                                                                                                                                                         62 GCACAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRY------ 110
                                                                                                                                                                                                                                                                                                                                                                           --GRELRRMADEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVF--- 151
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PSEQEDSSSAERGLGPSP--AGDGPSGSGKHHRQAPGLL----WDASHQQEQPTSSSHH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                       63;
                                                                   Length 1729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1300;
                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AGAVEIRSRHSSYPAGTEDDEGMGEE-----PSPFRGRSRSAP 101
                                                                                                                       :99
                                                                      5;
                                                                                                8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 93; DB
ilarity 29.0%; Pred. No. 8;
Conservative 6; Mismatches
                                                                                                                    23; Mismatches
                                                                   Score 94.5;
Pred. No. 8.
                                                                   10.48;
21.68;
                                                                                                                    42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1087 SVEKTPQQTWWEAN 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 ----- QSWWDRN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match'
Best Local Similarity
Matches 31; Conserv
                                                                                                Local Similarity
A; Note: var-2
                                                                      Query Match
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hypothetical protein 155R - Molluscum contagiosum virus 1
N;Alternate names: MC155R
C;Species: Molluscum contagiosum virus 1
C;Species: Molluscum contagiosum virus 1
C;Date: O5-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C;Accession: T30757
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Schence 273, 813-816, 1996
A;Tile: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host A;Reference number: Z20876; MUID:96325459
A;Accession: T3057
A;Accession: T3057
A;Accession: T3057
A;Accession: T3057
A;Accession: T3057
A;Accession: Pape: DNA
A;Mesidus: 1-336 <SEN>
A;Residues: 1-336 <SEN>
A;Cross references: EMBL:U60315; PIDN:AAC55283.1
                                                                                                                                                             Cippecies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacie : 04-War - 1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
Cipacie : 04-War - 1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
Cipacies: 04-War - 1992
Science 257, 389-395, 1992
A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-A:Title: Structure and functional expression of an omega-conotoxin-sensitive human N-A:Reference number: A42566; MUID:92339886
A:Reference number: A42566; MUID:92339886
A:Status: preliminary; not compared with conceptual translation
A:Residues: 1-2339 cWIL>
A:Residues: 1-2339 cWIL>
A:Residues: 1-2339 cWIL>
A:Residues: INR32, hippocampus
A:Experimental source: INR32, hippocampus
A:Experimental source extracted from WCBI backbone (NCBIP:109168)
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                          omega-conotoxin-sensitive N-type calcium channel alpha 1B-1 subunit (alternatively sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 IRSRHSSYPAGTEDDEGMGEEPSPFRG------RSRSAPPNLWAAQRYGRELR 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 -SHQQEQPTSSSHHGGAGAV-EIRSRHSSYP-AGTEDDEGMGEEPS-PFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 EPSEQED----SSSAERGLGPSPA-----GDGPSGSGKHHRQAPGLLWDA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 RMADE-FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.9%; Score 90; DB 2; Length 2339; 30.8%; Pred. No. 26; Live 16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score 89.5; Dl
30.1%; Pred. No. 3.6;
:ive 18; Mismatches
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Best Local Similarity 30.19
Matches 52; Conservative
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Best Local Similarity
Matches 36; Conserv
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Rivillians, M.E.; Brust, P.F.; Feldman, D.H.; Patthi, S.; Simerson, S.; Maroufi, A.; McC Science 257, 389-395, 1992
A; Title: Structure and functional expression of an omega-conotoxin-sensitive human N-typ A; Reference number: A42566; MUID:92335886
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2237 AMIL:
A; Residues: Call line IMR32; neuroblastoma
C; Genetics:
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Profitaggrin - human (fragments)
C: Species: Homo sapiens (man)
C: Species: Homo sapiens (man)
C: Species: Homo sapiens (man)
C: Date: 14-Dec-1990 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C; Accession: A35938
R; Gan, S.O.; MoBride, O.W.; Idler, W.W.; Markova, N.; Steinert, P.M.
Blochemistry 29, 9432-9440, 1990
A; Title: Organization, structure, and polymorphisms of the human profilaggrin gene.
A; Reference number: A35938; MUID:91064347
A; Reference number: A35938; MUID:91064347
A; Recession: A35938
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-2248 <GAN>
A; Cross-references: GB:10929
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Cross-references: GB:119912; OMIM:135940
C; Superfamily: unassigned calmodulin-related proteins; calmodulin repeat
C; Superfamily: unassigned calmodulin-related proteins; calmodulin repeat
C; Superfamily: unassigned calmodulin repeat
F; 20-6950/Region: filaggrin repeat
F; 1074-1397/Region: filaggrin repeat
F; 1074-1397/Region: filaggrin repeat
F; 1573-1896/Region: filaggrin repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 -SHQQEQPTSSSHHGGAGAV-EIRSRHSSYP-AGTEDDEGMGEEPS-PFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: calcium influx
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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Best Local Similarity 26.6%; Pred. No. 25;
Matches 38; Conservative 13; Mismatches 5(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.9%; Score 90; DB; Best Local Similarity 30.8%; Pred. No. 25; Matches 36; Conservative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C; Accession: 173049
R; Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
Submitted to the EMBL Data Library, March 1998
A; Reference number: 217592
A; Accession: T13049
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2715 < TRE>
A; Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMAD--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 --PLASLPSPKHPGPQAKEDSEGPSQGPA----SREKGLSAEQ--GRQTEREEEEEFK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 DPSIQQQQNVAPHPYGAPPPPGSGPGG-----PPGPDPAAVMHYHHLHQQQQQHPPPPP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 -- TSSSHHGGAGAVEIRSRHSSYPAGT-EDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Wg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 EFEPSEQE---DSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG
A;Title: Nature of the pH-induced conformational changes and exposure A;Reference number: S38976; MUID:94063061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
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A;Description: could act as a transcription factor antagonistic to
C;Keywords: DNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 WEEAEAREKAVPEEESPPTAAFKAPPSLGNKETORAAPGW 270
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Matches 42; Concernation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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9.8%; Score 88.5; DE
Best Local Similarity 24.4%; Pred. No. 5.9;
Matches 39; Conservative 19; Mismatches
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                        N'Alternate names: pituitary secretory protein I; secretory protein I N'Contains: chromostatin; pancreastatin C'Species: Bos primigenius taurus (cattle) C'Accession: A41520; A28033; A44175; A60306; A61114; S15847; S39016; I46008; S38976 R; Tacangelo, A.L.; Grimes, M.; Eiden, L.E. Mol. Endocrinol. 5, 1651-1660, 1991 A; Feference number: A41520; MUID: 92140395 A; Tettle: The bovine chromogranin A gene: structural basis for hormone regulation and gen A; Reference number: A41520; MUID: 92140395 A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: DNA
A: Residues: 1-449 < IAC.
A: Cohn, D.V.; Gorr, S.U.; Ornstein, D.L.; Kashdan, M.A.; Levine, M.A.
A: Cohn, D.V.; Gorr, S.U.; Ornstein, D.L.; Kashdan, M.A.; Levine, M.A.
A: Title: Primary structure of bovine pituitary secretory protein I (chromogranin A) dedu
A: Reference number: A20033, MUID: 87260925
A: Accession: A20033
A: Molecule type: MRNA
A: Residues: 1-111, T', 113-190, Y', 192-253, P', 255-378, R', 380-449 < AHN>
A: Residues: 1-111, T', 113-190, Y', 192-253, P', 255-378, R', 380-449 < AHN>
A: Residues: Translated the codon CGG for residue 391 as Gln
A: Mote: the authors translated the codon CGG for residue 391 as Gln
A: Mote: A: Affolter, H.U.; Eiden, L.E.; Herbert, E.; Grimes, M.
Nature 323, 82-86, 1986
A: Atitle: Bovine chromogranin A sequence and distribution of its messenger RNA in endocri
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A; Molecule type: protein
B; Residues: 19-34, Y, Y, 36-38, 97-111; 134-139 < BA2>
R; Residues: 19-34, Y, Y, 36-38, 97-111; 134-139 < BA2>
B; R; Residues: 1, 276, 471-479, 1991
Biochem. J. 276, 471-479, 1991
A; Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and act A; Reference number: $15847; MUID: 91264803
A; Accession: $15847
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A;Molecule type: protein
A;Residuae 330-331 <WAT>
R;Benedum, U.M.; Baeuerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.; Huttn
EMBO J. 5, 1495-1502, 1986
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A; Cross-references: EMBL:X04012; NID:g197; PIDN:CAA27636.1; PID:g198

R; Yoo, S. B.; Ferretti, J. A.

FEBS Lett. 334, 373-377, 1993
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A;Residues: 266-310, H' 312-318, K', 320-331 <WA2>
A;Residues: 266-310, H' 312-318, K', 320-331 <WA2>
A;Note: 311-347 and 319-Glu were also found
B;Watkinson, A.; Rogers, M.; Dockray, G.J.
Biochem. J. 295, 649-654, 1993
A;Title: Post-translational processing of chromogranin A: differential distribution of A;Reference number: S39016; MUID:94059013
A;Accession: S39016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Rosadiues: 1-153, 'PO', 156-158,' R', 160-190,' Y', 192-253,' P', 255-449 < IA2>
A; Cross-references: GB: X04298; NID: 9217; PIDN: CAA27841.1; PID: 9218
B; Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ishida, K.; Makk, G.; Angwin, P.; Chang, I Regul. Pept. 25, 207-213, 1989
A; Title: Isolation and characterization of bovine pancreastatin.
A; Reference number: A60306; MUID: 89331945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 266-312 <NAK>
R;Barbosa, J.A.; Gill, B.M.; Takiyyuddin, M.A.; O'Connor, D.T.
Endocrinology 128, 174-190, 1991
A;Title: Chromogranin A: posttranslational modifications in secretory granules.
A;Reference number: A61114; MUID:91099142
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       chromogranin A precursor [validated] - bovine
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A; Molecule type: protein
A; Residues: 567-580 A; Residues: 567-580 A; Residues: 567-580 A; Residues: 567-580 Coll.>
B; Yoo, S.H.
Biochia. Biophys. Acta 1179, 239-246, 1993
A; Title: pH-dependent binding of chromogranin B and secretory vesicle matrix proteins
A; Reference number: S39369; MUID: 94032431
A; Residues: 239-244; 562-565 A; Molecule type: protein
A; Residues: 239-244; 562-565 CYOO>
C; Superfamily: chromogranin B precursor
C; Keywords: adrenal gland; glycoprotein; pituitary; pyroglutamic acid; sulfoprotein
F; 1-20/Domain: signal sequence #status predicted <AMT>
F; 51-646/Product: chromogranin B #status predicted <AMT>
F; 567-580/Product: pyroglutamyl peptide BAM-1745 #status experimental <AM2>
F; 567-580/Proluct sales predicted
F; 36-57/Disulfide bonds: #status predicted
F; 315/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 315/Binding site: sulfate (Tyr) (covalent) #status predicted
F; 567/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF079764; NID:g3757889; FID:g3757890; PIDN:AAC64271.1
A;Experimental source: imaginal disc
C;Genetics:
A;Gene: E(PC)
A;Cross-references: FlyBase:FBgn0000581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 PGESEEDA-----SPEVDKRHSRPRHHGRSRP----DRSSQEGNPPLEEESHVGTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGR-----ELRRMA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAVEIRSRHSSYPAGTEDDEGMG---EEPSPFRGRSRSAPPNLWAAQRYGRELRRMAD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 KLPRDKQQHQQQQTQQHQQQQYLPASGGAGVSPAHH--LPHHLHHLSRQQ-----SASPA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH--RQAPGLLWDASHQQEQP--TSSSHHGGA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.6%; Score 87; DB 1; Length 646; Best Local Similarity 27.9%; Pred. No. 11; Matches 36; Conservative 17; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 DEFVDSFKK 127
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A; Residues: 1-646 <BIO>
A; Cross-references: EMBL:X55027; NID:g11; PIDN:CAA38846.1; PID:g12
A; Grandy, D.K.; Leduc, R.; Makam, H.; Flanagan, T.; Diliberto, E.J.; Thomas, G.; Civelli Submitted to the EMBL Data Library, October 1990
A; Description: Nucleotide and deduced amino acid sequence of bovine adrenal medulla Chroman A; Reference number: S20727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 567-580 <FLAS
R;Billen, L.; Boel, S.; de Potter, W.P.; Claeys, M.
Biochim. Biophys. Acta 1120, 105-112, 1992
A;Title: Mass spectrometric characterization of bovine chromaffin granule peptides relat
A;Reference number: S21773; MUID:92207983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: $20027
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuaes: 21-63, N', 65-92, FRS', 96, 'RA', 99-100, 'S', 101-480, 'L', 482-646 <GRA>
A; Cross-references: EMBL: X5489; NID: 9201; PIDN: CAA39109.1; PID: 9202
B; Flanagan, T.; Taylor, L.; Poulter, L.; Viveros, O.H.; Diliberto Jr., E.J.
A; Flanagan, T.; Taylor, L.; Poulter, L.; Viveros, O.H.; Diliberto Jr., E.J.
A; Flile: A novel 1745-Dalton pyroglutamyl peptide derived from chromogranin B is in the A; Accession: A61076; MUID: 91223542
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: Si5901; S20727; A61076; S21773; S39369
R;Bauer, J.W.; Fischer-Colbrie, R.
Biochim. Biophys. Acta 1089, 124-126, 1991
A;Title: Primary structure of bovine chromogranin B deduced from cDNA sequence. A;Reference number: Si5901; MUID:91223091
                                                                                                                                                                                        C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C; Accession: T43500
A; Reference number: 22515
A; Accession: T43500
A; Accession: T43500
A; Residues: 1-222 AAAA>
A; Residues: 1-222 AAAA>
A; Residues: 1-222 AAAA>
A; Cross-references: EMBL:AL133642
A; Cross-references: EMBL:AL133642
A; Experimental source: adult uterus; clone DKF2p586G1721
C; Genetics: Description of the properties of the propert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 ------HSSYPAGTEDDEGMGEEP--SPFRG-RSRSAPPNLWAAQRYGRELRRMAD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 EDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 222;
                                                                                                                                                                hypothetical protein DKF2p586G1721.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.7%; Score 88; 27.3%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Note: DKFZp586G1721.1
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Attender ich protein hairless - fruit fly (Drosophila melanogaster)
N:Alternate names: 109K basic protein H
C;Species: Drosophila melanogaster
C;Date: 10-Jun-1993 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999
C;Accession: A44667; A58929; S33412; S24639
R;Bang, A.G.; Posakony, J.W.
Genes Dev. 6, 1752-1769, 1992
A;Title: The Drosophila gene Hairless encodes a novel basic protein that controls altern A;Reference number: A44067; MUID:92387549
A;Accession: A44067
A;Residues: 19-107
A;Residues: 19-107
A;Residues: 19-107
A;Coss references: GB:M95192; NID:g157621; PID:g157622
A;Cross reference extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riversis, A. submitted to the EMBL Data Library, May 1994
A. Rescitation number: A58929
A. Recession: A58929
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-1077 < ARE>
A. Kollecule type: mRNA
A. Residues: 1-1077 < ARE>
A. Cross references: EMBL. X67239; GB:S49642; NID:g578331; PID:g578332
B. Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
Mech. Dev. 38, 143-156, 1992
Mech. Dev. 38, 143-156, 1992
Mech. Dev. 38, 143-156, 1992
A. Rittle: Hairless, a Drosophila gene involved in neural development, encodes a novel, se A. Reference number: S33412; MoID:93041287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;MOlecule type: mRNA
A;Residues: 1-150,'A',152-701,'LL',704-890,'R',892-963,'RLLP',968-973,975-1077 <MAI>A;Cross-references: EMBL:X67239
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Best Local Similarity 28.9%; Pred. No. 22;
Matches 37; Conservative 17; Mismatches 47; Indels 27; Gaps
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    ---RRLGRG 520
482 E--DMAPSGACSDAKYRYTLTSLNYPRPRCIGFAR---
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Search completed: October 9, 2001, 15:58:10 Job time: 35 sec

722 KSPDVSGS--NGGGGKSPSHTGTKKRSPPYSAGSPVDYGHSFYR--DPYA----GAGRP 772

133 KSAGTATQ 140 ::|:|:| STSGSASQ 780

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773

73 HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEFVDSFKKGLPRP 132

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2001, 16:03:43; Search time 15.11 Seconds (without alignments) 380.868 Million cell updates/sec Run on:

09-580523-1B 905 1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	Description	4 homo sapien	mus m		neuro	5 homo sapien	bos t		homo sapien	drosc		2 homo sapien	bos taurus	рошо	mns mnscnjn		2 homo sapien	gall	5 mus musculu	pos	homo	homo	homod	drosc	sdna	8 mus musculu	arabidopsis		3 craterostig		7 homo sapien	murine	gallus	8 homo sapien
	escr	09293	~	ın	001631	00097	05059	P2338	000192	02308	1167	P5153	095120	012809	P0902	06092	P5055	004584	P3041	P0121	P2071	096013	P14866	096433	P5501	P1108	000958	4942			_	069154	^,	013428
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di	Ouery Match	81.9	71.4	10.7		6.6	٠	•	•			•	4.6	9.4		9.3	9.3		٠	9.5		•	9.1	9.1	٠	9.1	9.1		٠	•	٠	9.0		g.
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P20659 drosophila P23771 homo sapien	P36787 human papil Q63003 rattus norv	Q05152 oryctolagus	015117 homo sapien 09y6j0 homo sapien	P08462 rattus norv P98193 rattus norv	P51514 rattus norv
TRX_DROME GAT3_HUMAN	VE2_HPV25 5E5_RAT	CCAB_RABIT	FYB_HUMAN CABI_HUMAN	GRPB_RAT DMP1_RAT	HTF4_RAT
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80.5	088	80	79.5	79 79	79
34	37	0 0 0	417	<b>4</b> 4	45

## ALIGNMENTS

BAD_HU	BAD_HUMAN
QI.	BAD_HUMAN STANDARD; PRT; 168 AA.
S E	3.0
55	OI-NOV-1997 (MEI. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update)
5	(Rel 40.
DE	(BCL-2 BINDING COMPONENT (
S.	BAD OR BBC6 OR BCL2L8.
SO	
8	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ပ္ပ	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ŏ	NCBL_TaxID=9606;
X C	
ž :	SEQUENCE FROM N.A.
ž 5	111 D.A., bl 2., Hadig B., Chen S., 2100 H.; Sibmitted /MOV-1066 to the EWED S., Chone 1
ع <u>د</u>	SUBJETCHER (NOV-1990) TO THE EMBLYCHOUSE GARDSBESS. FINCHION DROMOTES CFII DEATH SHOFFSSENIII ONDESTEE FOR THE
3 5	BINDING TO BOLL-X(L) AND BOLL-2, THEREBY APPENDING THE LEVE
ဗ္ဗ	HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
ပ္ပ	THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2
ပ္ပ	
ပ္ပင္ပ	-!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
ع د	
3 2	-! SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1)
ပ္ပ	SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2
ပ္ပ	
ပ္ပ	
ပ္ပ	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ မ	between the Swiss Institute of Bloinformatics and the EMBL outsation -
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3 5	ace of non-protections as tong as test to the no and for commercial and this statement is not removed lisase by and for commercial
ر د د	modified use this scattering is not temporary of any tot commetter.  entities requires a license agreement (see bitto://www.ish-sib.ch/announce)
3 5	contract dequited a tirense agreement (see help.//www.isb sib.cm/ammounce or send an email to license@isb-eib.cm/ammounce
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DR	EMBL; U66879; AAB36516.1;
DR	MIM; 603167;
ΚW	Apoptosis.
FT	101 121
FI	146 163 BH2.
čS.	SEQUENCE 168 AA; 18408 MW; BDF3D99587C222BE CRC64;
O E	Query Match 81.9%; Score 741; DB 1; Length 168; Best Local Similarity 84.5%; Pred. No. 1.48-49;
Ψ	vative 1; Mis
Qy	1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
QQ	1 MEQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
δy	61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRWADE 120
QQ	61 HGGRWGCGDPESPQLLPRGDGGRRRDGGGAQPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120

Ellis S.B.

Euteleostomi;

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BAD\_MOUSE

δ g BAD

11D
DD41D
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97053792; PubMed=8898206; Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J., Hoffman S.M.G., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E., Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H., Ferrari M.D., Frants R.R.; Ferrari M.D., Frants R.R.; Ferrari m.D., Frants R.R.; Ferrari m.D., Frants R.R.; mutations in the Ca2+ channel gene CACNLIA4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMET. Cell Mol. Genet. 21:279-284(1995).

-!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED ENTRY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROPRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A GIVES RISE TO P AND/OR O-TYPE CALCIUM CURRENTS. PA'O-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA), THEY ARE HOWEVER INSENSITIVE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E., McInnis M.G., Ross C.A.; "Characterization of cDNA clones containing CCA trinucleotide repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W., Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.; "Autosomal dominant cerebellar ataxia (SCA6) associated with small polyglutamine expansions in the alpha IA-voltage-dependent calcium channel."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lung carcinoma;
MEDLINE=95123449; PubMed=7823133;
MEDLINE=95123449; PubMed=7823133;
MEDLINE=95123449; PubMed=7823133;
MEDLINE=95123449; PubMed=7823133;
MEXPRESSION and antibody inhibition of P-type calcium channels in human small-cell lung carcinoma cells.";
J. Neurosci. 15:274-283(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                            Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S. Harpold M.M., Johnson E.C., Williams M.E.;
"Structural elements in domain IV that influence biophysical and pharmacological properties of human alphalA-containing high-voltage-activated calcium channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-
000555; 092690; 016290; 099790; 099791; 099792; 099793; P78510;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2)
                                                                                                                                                                                                                                  Homo sapiens (Human).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                       CACNAIA OR CACNLIA4 OR CACH4 OR CACN3.
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Neuron;
MEDLINE=99158614; PubMed=10049321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=97141920; PubMed=8988170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Frontal cortex;
MEDLINE=96102310; PubMed=8525433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2038-2258 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1693-1807 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nat. Genet. 15:62-69(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived from human brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 87:543-552(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                  (BI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-ELL BULZDI-ZUYL(1292).

-1- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.

-1- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L), AND BCL-2, BUT NOT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J. "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 HGGAGAMETRSRHSSYPACTEEDEGMEEELSPFRGRSRSAPPNIMAAQRYGRELRRMSDE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.4%; Score 646; DB 1; Length 204; Best Local Similarity 75.0%; Pred. No. 2.4e-42; Matches 126; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                     121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6C2BA910205053F7 CRC64;
                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2505 AA.
                                                                                                                                                                                                       204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain, and Thymus;
MEDLINE=95136361; PubMed=7834748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L37296; AAA64465.1; -.
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1096330; Bad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 80:285-291(1995)
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                          OR BBC6
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ID CCAA_HUMAN
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                                                                                                                                                                                                       BAD_MOUSE
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DOMAIN

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RESULT.

158

PRINTS; PR00167; CACHANNEL

UNKED BY A 1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE POREPORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY. THE CHANNEL SUBUNITS BY ALPHA-2/DELTA
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

-1. SUBCELLUARA LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1. ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFONAS; BI-1/(V2), BI-1/(V2),
BI-1-GGCAG/IA-1 (SHOWN HERE), BI-1/(V1)-GGCAG, BI-1/(V2), BI-1/(V2)

-1. TISSUE SPECIFICITY: BRAIN-SPECIFIC; MAINLY FOUND IN CEREBRAL CORFEX, THALAMUS AND HYDOTHALAMUS. NO EXPRESSION IN
PREDMINNITY PRIVED WINCLE. PURKINJE CELLS CONTAIN
PREDMINNITY PLYPE VOCC, THE O'TYPE BEING A PROMINENT CALCIUM
CURRENT IN CEREBELLAR GRANULE CELLS.

-1. DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
PURDROPHOLIC TRANSMEMBRANE SEGMENTS (SI, \$2, \$3, \$5, \$6) AND ONE
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGES AFRANCERIZED BY A
SERIES OF POSITIVELY CHARGES AFRANCE AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGES AFRANCE AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AFRANCE AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AFRONCE. AT EVERY THIRD POSITION. POLYMORPHISM: THE POLY-GLN REGION OF CACNALA IS POLYMORPHIC: 6 TO TREPEATS IN THE NORMAL POPULATION, EXPANDED TO ABOUT 21 TO 30 REPRATS IN SPINOCERREBELLAR ATAXIA 6 (SCA6) PATIENTS. THERE SEEMS TO BE A CORRELATION BETWEEN THE REPRAT NUMBER AND EARLIER ONSET OF COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS THE DISORDER + <u>:</u> 

DISEASE: EXPANSION OF A CAG REPEAT IN THE CODING REGION OF CACNAIA IS THE CAUSE OF ONE FORM OF SPINOCEREBELLAR ATAXIA 6 (SCA6), AN AUTOSOWAL DOMINNAT DISORDER CHRRACTERIZED BY SLOWLY PROGRESSIVE CEREBELLAR ATAXIA OF THE LIMBS AND GAIT, DYSAPTHRIA, NYSTAGWUS, AND MILD VIBRATORY AND PROPRICCEPTIVE SENSORY LOSS. THESE SYMPTOMS ARE PROBABLY EXPLAINED BY SEVERE LOSS OF CEREBELLAR PURKINJE

DISEASE: DEPECTS IN CACNAIA ARE THE CAUSE OF FAMILIAL HEMIPLEGIC MIGRAINE (FHM), ALSO KNOWN AS MIGRAINE FAMILIAL HEMIPLEGIC I (MHPI), EPISODIC ATAXIA TYPE 2 (EA-2), ACETAZOLAMIDE-RESPONSIVE HEREDITARY PAROXYSMAL CEREBELLAR ATAXIA (APCA), AND POSSIBLY OTHER COMMUN TYPES OF MIGRAINES. FHM, A RARE AUTOSOWAL DOMINARY SUBTYPE OF MIGRAINE WITH AURA, IS ASSOCIATED WITH ICTAL HEMIPARESIS AND, IN SOME FAMILIES, PROGRESSIVE CEREBELLAR ATROPHY. EA-2 IS ANDTHER AUTOSOMAL DOMINANT PAROXYSMAL CEREBELLAR ATROPHY. EA-2 IS ANOTHER BUTOSOMAL DOMINANT PAROXYSMAL CEREBRAL DISEASE, CHARACTERIZED BY ACETOZOLAMIDE-RESPONSIVE ATTACKS OF CEREBELLAR ATAXIA AND MIGRAINE-LIKE SYMPTOMS, INTERICTAL NYSTAGMUS, AND CEREBELLAR ---

SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS ATROPHY FAMILY. This SWISS-PROT entry is copyright. It is produced through a collaboration modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch). EMBL outstation There are no restrictions on ng as its content is in no between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its conten

079663; AAB49674.1; ALT\_INIT. 079664; AAB49675.1; ALT\_INIT. 079667; AAB49676.1; ALT\_INIT. 079667; AAB49677.1; ALT\_INIT. Z80114; -; NOT\_ANNOTATED\_CDS. Z80115; -; NOT\_ANNOTATED\_CDS. U79666; AAB64179.1; -. EMBL; AF004884; AAB61613.1; -. EMBL; AF004883; AAB61612.1; -. X99897; CAA68172.1; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

S76537; AAB33068.1; -. U06702; -; NOT\_ANNOTATED\_CDS 601011; 183086; EMBL; EMBL; EMBL;

InterPro; IPR000636; -.
InterPro; IPR002077; -.
Pfam; PF00520; ion\_trans; 4.

2477 PA--HGLARPRGPGSRKGLHEPYS 2498

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Calcium channel, Glycoprotein, Repeat, Multigene family, Calcium-binding, Phosphorylation, Alternative splicing; Polymorphism, Disease mutation, Triplet repeat expansion. Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; EXTRACELLULAR (POTENTIAL).
S4 OF REPEAT II (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
S5 OF REPEAT II (POTENTIAL).
S6 OF REPEAT II (POTENTIAL).
S6 OF REPEAT II (POTENTIAL).
S6 OF REPEAT III (POTENTIAL).
S1 OF REPEAT III (POTENTIAL).
S1 OF REPEAT III (POTENTIAL).
S2 OF REPEAT III (POTENTIAL). CYTOPLASMIC (POTENTIAL). S5 OF REPEAT III (POTENTIAL). EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). S3 OF REPEAT III (POTENTIAL) S4 OF REPEAT III (POTENTIAL) S6 OF REPEAT III (POTENTIAL) S3 OF REPEAT IV (POTENTIAL). EXTRACELLULAR (POTENTIAL). S4 OF REPEAT IV (POTENTIAL). EXTRACELULAR (POTEWIAL).
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CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT II (POTENTIAL). CYTOPLASMIC (POTENTIAL). S1 OF REPEAT IV (POTENTIAL). S2 OF REPEAT IV (POTENTIAL). CYTOPLASMIC (POTENTIAL). S6 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL). CYTOPLASMIC (POTENTIAL). S5 OF REPEAT I (POTENTIAL). EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). S3 OF REPEAT I (POTENTIAL) (POTENTIAL) SI OF REPEAT I (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) (POTENTIAL) S4 OF REPEAT I S2 OF REPEAT I 1484 1509 1564 3335 3487 521 541 568 1297 1309 1328 1339 1358 1397 DOMAIN TRANSMEM FRANSMEM TRANSMEM TRANSMEM TRANSMEM **TRANSMEM** FRANSMEM FRANSMEM TRANSMEM TRANSMEM **FRANSMEM** TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM REPEAT REPEAT REPEAT DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN REPEAT DOMAIN DOMAIN 

11; 2373 PARSESPRACRHGGARWPASGPHVSEGPPGPRHHG------YYRGSDYDEADG 2419 2313 PQQQQQQQQQQAVARPGRAATSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPG 2372 ---GMGEE-----PSPFR-----GRS----RSAPPNLWAAQRYGRELRRMADEFV 122 Gaps -----GLLWDAS--HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE---80; DB 1; Length 2505; 5 PEFEPSEQED-----SSSAERGLGPSP---AGDGPSGSGKHHRQAP 22; Mismatches 54; Indels Score 97; Pred. No. 7 DSFKKGLPRPKSAGTATQMRQSSS 146 10.7%; 23.5%; Local Similarity 23.5 nes 48; Conservative Query Match 43 Matches 82 ò 셤 q δ g à ò

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TISSUE-Brain;
                                                                                                                                                                                                                                     CCAB_HUMAN
Q00975;
        SEQUENCE
                                  Query Match
                                           Best Local
DOMAIN
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                                                   Matches
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                Kore-Eda S., Murayama T., Uno I.;
"Isolation and characterization of the adenylate cyclase structural gene of Neurospora crassa.";
Jpn. J. Genet. 66:317-334(1991).
-!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                  01-JUL-1193 (Rel. 26, Created)
1-JUL-1993 (Rel. 26, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
ADENYLATE CYCLASE (EC. 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                                                            -1- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
-1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
-1- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
-1- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
                                                                                                      Neurospora crassa.
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                     Leucine-rich repeat; cAMP synthesis; Magnesium.
                                 2300 AA.
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00560; LRR; 13.
Pfam; PF00481; PP2C; 1.
PRINES; PR00019; LEWILCHRPT.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
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CATALYTIC.
POLY-SER.
                                PRT;
                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-92000795; Pubmed-1680356;
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LRR
LRR
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                                 STANDARD;
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                                                                                              CR-1 OR NAC.
                                 CYAA_NEUCR
                                                                                     CYCLASE)
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM DEPRENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORNONE OR BUBNOTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-AGA-ILIA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-AGA-IVA).

CALCIUM CHANNELS CONTAILING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
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SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-1, BETA AND DELTA SUBUNITS
IN A 1:1:1:1 RATIO: THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT: IN MANY CASES, THIS
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CHANNEL ACTIVITY: THE ANXILLARY SUBUNITS BETA AND ALPHA-2/DELTA
LINNED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34). Last sequence update)
01-0CT-2000 (Rel. 40). Last annotation update)
voltage.Dependent N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL CACNALB OR CACNLIA5 OR CACH5.
                                                                                                                                                                                                                                                                                                                                                               EIRSRHSS-----YPA-----GTEDDEGMGEEP-----SPFRGR---SRSA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 GGRDRDASPVPSRPRTPVPAPEVVPFLYQEADDIARYGEAPVRTSLTGPDRDRYIDSSQN 459
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                              17 SAERGLGPSPAGDGPSGSGKHHR----QAPGLLWDASHQQEQPTSSSHH-----GGAGAV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 PPKTSSSARSGHSIVHLPGHHKHNKSNEDPRALKPSLSREDSAASFARDFRNGSSSMMGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                  63;
                                                                                                                                                         Length 2300;
                                                                                                                                                                                                                                  74; Indels
                                    254752 MW; 52E79B90E6B17A7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPNLWAAQRYGREL - - - - - - RRMADEFVDSFKKGLPRPKSAGT - - -
                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2339 AA
                                                                                                                                                     10.1%; Score 91.5; D; 23.7%; Pred. No. 17; ive 24; Mismatches
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    POLY-GLN
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Science 257:389-395(1992).
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                                                                                                                                                                                                                                      50; Conservative
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        221
204 22
2300 AA;
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                                                                                                                                                                                                                                                                                                                      MIN; 601012; -.

MIN; 601012; -.

MIN; 601012; -.

MIN; 601012; -.

MIN; 60102077; -.

MIN; 601020077; -.

MIN; 60102 channel; 601 trans; 4.

PRINTS; PRO0167; CACHANNEL.

MIN; 6010 channel; 7 cachannel; 100 transport; Voltage-gated channel;

MIN; 6010 channel; 7 cachannel; 100 transport; Voltage-gated channel;

MIN; 6010 channel; 7 cachannel; 100 transport; Voltage-gated channel;

MIN; 6010 channel; 61ycoprotein; Repeat; Multigene family;

MIN; 6010 channel; 61ycoprotein; 61yco
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1B-1 (SHOWN HERE) AND
ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE
CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTH.
DOMAIN: EACH OF THE FOUR INTERRAL REPEATS CONTAINS FIVE
HYDROPHOBIC TRANSMEMBRANE SEGMENTS (51, 52, 53, 55, 56) AND ONE
POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (54). S4 SEGMENTS
PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
                                                                                                                                                                                                                                                  (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
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S4 OF REPEAT I (POTENTIAL).

S5 OF REPEAT I (POTENTIAL).

S5 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S1 OF REPEAT II (POTENTIAL).

S1 OF REPEAT II (POTENTIAL).

S2 OF REPEAT II (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S4 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

S6 OF REPEAT II (POTENTIAL).

S7 OF REPEAT III (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S7 OF REPEAT III (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S7 OF REPEAT III (POTENTIAL).

STOPPLASMIC (POTENTIAL).
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S3 OF REPEAT III (POTENTIAL).
EXTRACELLLILAR (POTENTIAL).
S4 OF REPEAT III (POTENTIAL).
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S5 OF REPEAT III (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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1392 1416 S6 OF REPEAT III (POTENTIAL). 1417 1471 CYTOPLASMIC (POTENTIAL). 1490 S1 OF REPEAT IV (POTENTIAL). 1506 1525 S2 OF REPEAT IV (POTENTIAL). 1526 1533 CYTOPLASMIC (POTENTIAL). 1553 1563 EXTRACELLUIAR (POTENTIAL). 1553 1563 EXTRACELLUIAR (POTENTIAL). 1553 1563 EXTRACELLUIAR (POTENTIAL). 1560 1560 EXTRACELLUIAR (POTENTIAL). 1561 S4 1560 S4 OF REPEAT IV (POTENTIAL). 1602 1621 S5 OF REPEAT IV (POTENTIAL). 1602 1631 EXTRACELLUIAR (POTENTIAL). 1603 1631 EXTRACELLUIAR (POTENTIAL). 1604 1708 S6 OF REPEAT IV (POTENTIAL). 1709 2339 CYTOPLASMIC (POTENTIAL). 1709 2339 POLY ** HIS.	396 458 314 663 1365 1655	BY SIMILARITY.  N-LINKED (GLCNAC)  N-LINKED (GLCNAC)  N-LINKED (GLCNAC)  GSGSVNGSPLISTSAFANSSPIFFAGAOTSI  OPLACSRISSPYLSTER  NSGRSSRTSYVSSLTS  RSYHPEDOBWC ->  ALELALTLYNGSSWYN  PGLPTCPP (IN ISC  MW; 17A45C6D1E7	tch al Similarity 30.8%; Score 90; DB 1; Length 2339; al Similarity 30.8%; Pred. No. 22; 36; Conservative 16; Mismatches 35; Indels 30; Gaps EPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLMDA	STANDARD; PRT; 449 AA. 79392; 87 (Rel. 05, Created) 88 (Rel. 09, Last sequence update) 800 (Rel. 40, Last annotation update) 800 (Rel. 40, Last annotation update) 800 (Rel. 40, Last annotation update) 807 (Rel. 40, Last an
TRANSMEM DOMAIN DOMAIN	DOMAIN NP_BIND SITE SITE SITE SITE SITE	CALBIND CARBOHYD CARBOHYD CARBOHYD CARBOHYD VARSPLIC SEQUENCE	Query Match Best Local Simil Matches 36, C 8 EPSEQED- 1   1   1   878 EPGREER 49 -SHQQEQP 1   1   1   936 RAHRHQDP	LT 6 BOVIN CMGA_BOVIN CMGA_BOVIN P05059; P7 13-AUG-196 01-NOV-196 CHCONGRAP CHROMOGRAP 14; CATEST CHA BOS taurus EUKATYOTA MAMMMALIA; MAMMMALIA; MAMMMALIA; MAMMMALIA; MAMMMALIA; MAMMMALIA; MAMMMALIA; MAMMMALIA; MAMMALIA; MAMMA
			DD	RESULT CMGA_B CMGA_B CMGA_B CD DT DT DD

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NCBI\_TaxID=9913; [1] SEQUENCE FROM N.A MEDLINE=97439785; PubMed=9294131;

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MEDLINE-86311345; PubMed=3018587; Iacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.; Machine chromogranin A sequence and distribution of its messenger RNA in endocrine tissues."; Nature 323:82-86(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoo S.H., Albanesi J.P.; "Ca2(+)-induced conformational change and aggregation of chromogranin
                                                                                           Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J., Mallet J., Huttner W.B.;
"The primary structure of bovine chromogranin A: a representative of a class of acidic secretory proteins common to a variety of peptidergic cells.";
EMBO J. 5:1495-1502(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M., van Dorsselaer A., Aunis D., Metz-Boutigue M., H., H., "Antibacterial activity of glycosylated and phosphorylated chromogranin A-derived peptide 173-194 from bovine adrenal medullary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89331945; Pubmed-2756155;
Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,
Chang D., Tatemoto K.;
                                                                                                                                                                                                                                                                                                                                                                                    Kang Y.K., Yoo S.H.;
"Identification of the secretory vesicle membrane binding region of
chromogranin A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galindo E., Rill A., Bader M.-F., Aunis D.; "Chromostatin, a 20-amino acid peptide derived from chromogranin A, inhibits chromaffin cell secretion."; Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
          Iacangelo A.L., Grimes M., Eiden L.E.;
"The bovine chromogranin A gene: structural basis for hormone
regulation and generation of biologically active peptides.";
Mol. Endocrinol. 5.1651-1660(1991).
                                                                                                                                                                                                                                                                                           T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
                                                                                                                                                                                                                                                                                                                "Primary structure of bovine pituitary secretory protein I (chromogranin A) deduced from the cDNA sequence."; Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and characterization of bovine pancreastatin."; Regul. Pept. 25:207-213(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galindo E., Rill A., Bader M.-F., Aunis D.;
Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 19-45, AND CALCIUM-BINDING.
MEDLINE-90354431; Pubmed-2387861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J: Biol. Chem. 271:28533-28540(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 265:14414-14421(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Chromaffin granules;
MEDLINE=97067080; PubMed=8910482;
                                                                                  MEDLINE-86300648; PubMed-3755681;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97228583; Pubmed=9074643;
 MEDLINE=92140395; PubMed=1779968;
                                                                                                                                                                                                                                                                              MEDLINE=87260925; PubMed=3474638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 191-212 (CHROMACIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF CATESTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 404:87-90(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 266-312.
                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                       Levine M.A.;
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Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H., Gill B.M., Parmer R.J., "Novel autocrine feedback control of catecholamine release. A discrete chromogranin a fragment is a noncompetitive nicotinic cholinergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUNCITON: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM CHROMAFFIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-COMPETITIVE NICOTINIC CHOLLINERGIC ANTAGONIST.
FUNCTION: VASOSTATIN-I HAS ANTIBACTERIAL ACTIVITY AGAINST GRAMPOSITIVE BACTERIA M.LUTEUS, B.SUBTILIS, S.PYROGENES, M.FORTUTUM, S.ANTEUS BACTERIA B.CEREUS, B.SUBTILIS, S.PYROGENES, M.FORTUTUM, E.COLI, E.CLOACAE, S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURUGINOSA. POSSESSES ANTIFUNGAL S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURUGINOSA. POSSESSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.FUBMIGATUS, A.BRASSICOLA, N.HEMATOCOCCA, F.CULMORUM AND F.OXYPORUM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99025667; PubMed-9809795;
MEDLINE-99025667; PubMed-9809795;
Tsigelny I., Mahata S.R., Taupone L., Preece N.E., Mahata M.,
Khan I., Parmer R.J., O'Connor D.T.;
"Mechanism of action of chromogranin A on catecholamine release:
molecular modeling of the catestatin region reveals a beta-
strand/loop/beta-strand structure secured by hydrophobic interactions
and predictive of activity:
Regul. Pept. 77:43-53(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CABÓHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
MEDLINE=99459228; PubMed=10527498;
Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
"Chromogranin A from bovine adreal medulla: molecular
characterization of glycosylations, phosphorylations, and sequence
heterogeneities by mass spectrometry.";
hall Biochem. 274:69-80(1999).
- I- FUNCTION: PANKEASTRAIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN
RELEASE FROM THE PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE FROM CHROMAFFIN CELLS.
                                                                                                                                                                                                                                                                                                                                              MEDLINE-99000113; PubMed-9786174;
Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
"Mechanism of cardiovascular actions of the chromogranin A fragment
catestatin in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASS SPECTROMETRY: MW-8584.9; METHOD-MALDI; RANGE-19-94.
MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20219105; PubMed=10753865;
Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
Aunis D., Metz-Boutigue M.-H.;
"Antibacterial and antifungal activities of vasostatin-1, the N-
terminal fragment of chromogranin A.";
J. Biol. Chem. 275:10745-10753(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.MENTAGROPHYTES.
SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAINST S.CEREVIASE AND C.ALBICANS YEAST. INACTIVE AGAINST
                                                                                                                                                                                                                     Clin. Invest. 100:1623-1633(1997).
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                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION OF CATESTATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides 19:1241-1248(1998).
                                                                                                                                                                                         antagonist.";
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TISSUE=Adrenal chromaffin;
                                                              SEQUENCE FROM N.A.
                                      sequence."
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DISULFID
MOD_RES
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8
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                                                                                                                                                                                                                                                                                                                                                                                                             138 EVEKSDEDSDGDRPQASPGLGPGP-----KVEEDNQAPG------EEEEAPSNAH-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 --PLASLPSPKYPGPQAKEDSEGPSQGPA----SREKGLSAEQ--GROTEREEEEEK 230
                                                                                                                                                                                                                                                                                                                                                                            45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            6 EFEPSEQE---DSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG 62
                                                                                                                                                                     pfam; PF01271; Granin; 1.
PRINTS; PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS_1; 1.
PROSITE; PS00423; GRANINS_2; 1.
Signal; Amidation; Glycoprotein; Calcium-binding; Phosphorylation; Polymorphism; 3D-structure; Antibiotic; Fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SG1_BOVIN STANDARD; PRT; 646 AA.
SG1_BOVIN STANDARD; PRT; 646 AA.
D13389; 002707;
01-NOV-1991 (Rel. 20, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK CHGB.
                                                                                                                                                                                                                                                                                                                                                        ; Score 87.5; DB 1; Length 449;
; Pred. No. 6;
19; Mismatches 57; Indels 45
                                                                                                                                                                                                                                                                                         CATESTATIN.
PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION (PARTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 WEEAEAREKAVPEEESPPTAAFKPPPSLGNKETQRAAPGW 270
                                                                                                                                                                                                                                      CHROMOGRANIN A.
                                                                                                                                                                                                                                                                          PANCREASTATIN.
                                                                                                                                                                                                                                               VASOSTATIN-1.
CHROMOSTATIN.
                 579258; AAB21297.1; JOINED.
579260; AAB21297.1; JOINED.
579262; AAB21297.1; JOINED.
579264; AAB21297.1; JOINED.
579266; AAB21297.1; JOINED.
579268; AAB21297.1; JOINED.
                                                                     L; X04012; CAA27636.1; -...
L; X04298; CAA27841.1; -...
L; M16971; AAA30765.1; -...
L; U73523; AAC48700.1; -...
; A41520; A41520.
                                                                                                                                                                                                                                                                                                                                                         9.78;
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                                                                                                                          PIR; A28033; A28033.
PDB; ICFK; 22-MAR-99.
GlycoSultebB; P05059; -.
InterPro; IPR001819; -.
InterPro; IPR001909; -.
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 24.4%
Matches 39; Conservative
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SEQUENCE FROM N.A.
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19
142
191
266
334
362
142
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MEDLINE=95262699; PubMed=7744058;
MEDLINE=95262699; PubMed=7744058;
MEDLINE=95262699; PubMed=7744058;
MEDLINE=95262699; PubMed=7744058;
Marcasalaer A., Adnis D., Metz-Boutique M.-H.;
"Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolyth, the endogenous C-terminal fragment of residues 614-626 with antibacterial activity.";
Eur. J. Blochem. 229:356-368(1995).
                                                                                                                                                                                       TISSUE=Adrenal medulla;
MEDLINE=97282588; PubMed=9136897;
Yoo S.H., Kang Y.K.;
"Identification of the secretory vesicle membrane binding region of chromogranin B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: O-GLYCOSYLATED (PROBABLE).
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
FAMILY.
                                                    'Primary structure of bovine chromogranin B deduced from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto Thomas G., Civelli O., Viveros O.H.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulfatation; Cleavage on pair of basic residues; Signal.
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SECRETOLYTIN.
BY SIMILARITY.
SULFATATION (POTENTIAL).
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                                                                                                           Biochim. Biophys. Acta 1089:124-126(1991).
MEDLINE=91223091; PubMed=2025642;
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PRIMES; PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS.1: 1.
PROSITE; PS00423; GRANINS.2: 1.
                             Bauer J.W., Fischer-Colbrie R.
                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 406:259-262(1997).
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 21-646 FROM N.A.
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InterPro, IPR001819; ..
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Adrenal medulla;
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484
646
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158
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09-580523-1b.rsp

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Q02308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM AND A LONG FORM (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-! TISSUE SPECIFICITY: FOUND IN ALL THE EXAMINED TISSUES INCLUDING HEART BRAIN, LIVER AND KIDNEY. FOUND AT LOW LEVEL IN LUNG.
-!- DISEASE: GENE DELETED IN VELO-CARDIO-FACIAL SYNDROME (VCFS) AND IS HEMIXYGOUS IN ALL VCFS PATIENTS WITH INTERSITIAL DELETIONS. THIS HEMIXYGOSITY MAY PLAY A ROLE IN THE ETIOLOGY OF SOME OF THE PHENOTYPES ASSOCIATED WITH VCFS CHARACTERIZED BY A WIDE SPECTRUM PHENOTYPES, INCLUDING CONOTRUNCAL HEART DEFECTS, CLEFT PALATE AND FACIAL DYSMORPHOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97271559; PubMed=9126485;
MEDLINE=97271559; PubMed=9126485;
Sirotkin H., O'Donnell H., DasGupta R., Halford S., St Jore B.,
Puech A., Parimoo S., Morrow B., Skoultchi A., Weissman S.,
Scambler P., Kucherlapati R.;
"Identification of a new human catenin gene family member (ARVCF) from
the region deleted in velo-cardio-facial syndrome.";
Genomics 41:75-83(1997).
--- FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS AT ADHERENS
                                                                                                                                                                                                                                                                                                                                                                                   246 PGESEEDA-----SPEVDKRHSRPRHHHGRSRP----DRSSQEGNPPLEEESHVGTG 293
                                                                                                                                                                                                                                                                                                                                                                                                                           65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGR-----ELRRMA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Gaps
                                                                                                                                                                                                                                                                                                                                            9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHH--RQAPGLLWDASHQQEQP--TSSSHHGGA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ARMADILLO REPEAT PROTEIN DELETED IN VELO-CARDIO-FACIAL SYNDROME.
                                                               3)
                                                                                                                                                                                                                                                            DB 1; Length 646;
    SIMILARITY).
                                                                                                                                                                                                                                                                                                    Indels
                                                                 (IN REF.
                                                                                                                                                                                          420DB1178FD9E415 CRC64;
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                                                                                                                                                                                                                                                                                                  52;
                   N -> S (IN REF. 1).
N -> D (IN REF. 2).
SEAPGL -> FRSPRAS (
T -> M (IN REF. 2).
P -> R (IN REF. 2).
P -> R (IN REF. 2).
P -> R (IN REF. 2).
M -> V (IN REF. 3).
    SULFATATION (BY
                                                                                                                                                                                                                                                        Query Match 9.6%; Score 87; DB 1
Best Local Similarity 27.9%; Pred. No. 9.6;
Matches 36; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             962 AA.
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                                                                                                                                                                                             MM;
                                                                                                                                                                                             73339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
  315
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98
181
2261
386
481
315
64.
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261
386
481
597
646 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 EESLEQENK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 DEFVDSFKK 127
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MOD_RES
CONFLICT
CONFLICT
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                                                                                                                                                                                             SEQUENCE
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  SELLLLLES
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MEDCNVHSAASILASVKEQEARFERLTRALEQERRHVALQL
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bang A.G., Posakony J.W.;
"The brosophila gene Hairless encodes a novel basic protein that
controls alternative cell fates in adult sensory organ development.";
Genes Dev. 6:1752-1769(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 EIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE--LRRMADEFVDSF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 EPRDSPSYGSLSRGLGMRPPRAGPLGPGP----------------------------GDGCF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-93041287; PubMed=1419850;
Maier D., Stumm G., Kuhn K., Preiss A.;
"Hairless, a Drosophila gene involved in neural development, encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 EPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAV 67
                                                                                                                                                                                                                                                                                                                                                                         ERAQQPGMVSGGMGSGQPLPMAWQQLVL -> MPAELR (IN SHORT ISOFORM).
; 74A1814A022FF2B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                       COILED COIL (POTENTIAL).
NUCLEAR LOCALIZATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 87; DB 1; Length 962; 25.2%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 KKGLPR-PKSAGTATQMRQSSS---WTRVFQSWWD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 DEGGPELEPDYGTATRRPECGRGLHTRAYEDTAD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1077 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                     splicing.
                                                                                                                                                                        POLY-ARG.
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                                                                              Pram: PF00514; Armadillo_seg; 4. PROSITE; PS50176; ARM_REPEAT; 3. Repeat; Coiled coil; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a novel, serine rich protein."; Mech. Dev. 38:143-156(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 28, Created)
(Rel. 28, Last sequ
(Rel. 28, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                                                                                                                                                                                          104641
EMBL; U51269; AAC51202.1;
HSSP; Q02248; 2BCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                     623
611
387
429
508
622
686
686
738
738
781
826
69
                                                                  interPro; IPR000225;
                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                      608
348
390
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468
526
575
646
699
739
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                                               MIM; 192430;
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01-FEB-1994
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pseudorabies virus.";
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
FUNCTION: IS A POTENT ANTAGONIST OF NEUROGENIC GENE ACTIVITY DURING SENSORY ORGAN DEVELOPMENT. THE EXPRESSION OF DISTINCT CELL FATES BY THE TRICHOGEN (SHAFT) / TORMOGEN (SOCKET) SISTER CELL PAIR DEPENDS ON THE LEVEL OF A ACTIVITY. A CERTAIN THRESHOLD LEVEL OF H ACTIVITY. IS REQUIRED, BELOW WHICH BOTH SISTER CELLS ADOPT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEFVDSFKKGLPRP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSSSSG---KKCGDHPAAIISNVHHPQ-----HSMYQPSSSSYPRAL---LTSP 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 KSPDVSGS--NGGGGKSPSHTGTKKRSPPYSAGSPVDYGHSFYR--DPYA-----GAGRP 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSAERGLGPSPAGDGPSG--SGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSR 72
                                                                                                                         -i- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-i- TISSUE SPECIFICITY: OVARY, EMBRYOS, LARVAL AND PUPAL IMAGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheung A.K.; "DNA nucleotide sequence analysis of the immediate-early gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1077;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN RÈF. 2).
W; A94BF1A27579E2F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ALA.
ALA-RICH.
HIS/PRO-RICH (PRD MOTIF).
S -> A (IN REF. 2).
QH -> LL (IN REF. 2).
A -> R (IN REF. 2).
AAVA -> RLLP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r protein; DNA-binding.
THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.5; I
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                         SIMILARITY: CONTAINS A "PRD MOTIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M95192; AAA28607.1; ALT_INIT.
EMBL; X67239; CAA47664.1; -.
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MEDLINE-89315207; PubMed=2546124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein; Nuclear
DOMAIN 115 123 TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE-EARLY PROTEIN IE180.
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FlyBase; FBgn0001169; H.
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974
1008
151
703
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964
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1077 AA;
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773 STSGSASQ 780
                                                                                                         TORMOGEN FATE
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P11675;
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CONFLICT
SEQUENCE
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 PARRGPASPASPAAGPVSAPGGGGAPSGGGDRGRHHHQHREPLLDEPAAARRLDPRPLGA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 ASHQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEEPSPFRGRSRSAP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 RSPVSSNPNSSSSSTTTVAVEPVAR-----GPEKDEDGLGLAGDGGAPLQRQPRRRRAG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Khavari P.A., Peterson C.L., Tamkun J.W., Mendel D.B., Crabtree G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------APGLLWD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khavari P.A., Peterson C.L., Tamkun J.W., Mendel D.B., Crabtree G.R. "BRG1 contains a conserved domain of the SW12/SNF2 family necessary for normal mitchic growth and transcription.";
Mature 366:170-174(1993).
                                                                                            Cheung A.K.;
Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POSSTBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1
PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

390 405 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 PNLWAAQRYGRELRRMADEFVDS----FKKGLPRPKSAGTATQMRQSSS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 E---GALRRGRGFSSSSGGSDSDLSPARSPSAPRAPAAAAARRSASS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-SER,
Ww: 7F31E7ABE403B208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.5; DE
Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSEQEDSSSAERGLGP - - SPAGDG - PSGS - - - GKHHRQ -
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Nucleic Acids Res. 17:4637-4646(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149833 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X15120; CAA33214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1461 AA;
                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S04713; EDBEIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN HOMOLOG 1).
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                                                                 REVISIONS
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Best Local S
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 012809; 075680;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
VOLTAGE-GATED POTASSIUM CHANNEL HERG (POTASSIUM CHANNEL, VOLTAGE-GATED
SUBFAMILY H MEMBER 2) (ETHER-A-GO-GO-RELATED PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                               phosphoprotein gene.";
J. Dent. Res. 76:754-760(1997).

-I. FUNCTION: COULD BE INVOLVED IN THE INDUCTION OF MINERALIZATION OF EXTRACELLULAR MATRIX AND IN DENTINGENESIS.

-I. TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH PARTICULARLY IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 PSQENSSESQEEALHES-RGDNPDNATSHSRE-----HQADSESSEEDVLDKPSDS 396
                                                                                                                                                                                                                                                                                                                                               Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.; "Cloning and expression analysis of the bovine dentin matrix acidic
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

DENTIN MATRIX ACIDIC PHOSPHOPROTEIN

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ----QEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAP 101
                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1 PRECURSOR (DENTIN MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.4%; Score 85.5; DB 1; Length 510; 25.2%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                         IISSUE=Tooth;
MEDLINE=97263952; PubMed=9109824;
Transi-n'Connor K., Young M.F., Dixon M.J.;
Transian ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9BFA9A74F6450865 CRC64;
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                   510 AA
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                     PRT;
                                                           Created)
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                     . STANDARD;
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510
351
370
427
464
                                                         (Rel. 39, (Rel. 39, 1
                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
                                                                                                                                 PROTEIN-1) (DMP-1).
                                                                                                                                                                         Bos taurus (Bovine)
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427
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30-MAY-2000 (
30-MAY-2000 (
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                 DMP1_BOVIN
095120;
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AC 012809

DT 30-MAY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                         Chiba H., Muramatsu M., Nomoto A., Kato H.;
"Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and
Drosophila brahma are transcriptional coactivators cooperating with
the estrogen receptor and the retinoic acid receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Nuclear protein; Activator; Bromodomain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEQEDSSSAERGLGPSPAGDGPSGSGKHH---RQAP-GLLWDASHQQEQPTSSSHHGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: NUCLEAR.
-1- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-1- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLU.
W; 7B785E7953277F1D CRC64;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDDPRYNQMKGMGMRSGGHAGMGPPPSPMDQHSQGYPSPLGGSE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
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ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86.5;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-GLU.
BROMODOMAIN.
                                                                                                                                                   Nucleic Acids Res. 22:1815-1820(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
                                                     MEDLINE=94268902; PubMed=8208605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00176; SNF2_N; 1.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00271; helicase_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D26156; BAA05143.1; -. AC006127; AAC97987.1;
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InterPro; IPR001487; -.
InterPro; IPR001650; -.
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1547
1584
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Best Local Similarity
Matches 31; Conserv
                                   SEQUENCE FROM N.A.
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1477
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NP_BIND
SITE
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EMBL; EMBL; MIM;

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Gaps --- 51

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Indels

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DOMAIN

DOMAIN DOMAIN

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85

RESULT

(POTENTIAL)

SITE

Genet. 102:265-272(1998).

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MEDLINE-94211879; PubMed-8159766;
Warmke J.W., Ganetzky B.;
"A family of potassium channel genes related to eag in Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
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MEDLINE-97176600; PubMed-9024139;
Tanaka T., Nagai R., Tomolke H., Takata S., Yano K., Yabuta K.,
Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,
Nakamura Y.;
"Four novel KVLQT1 and four novel HERG mutations in familial long-QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS LQT2 LEU-612; VAL-614; ASP-629; SER-629 AND SER-633.
MEDLINE-98204197; Pubmed-9544837;
Satler C.A., Vesely M.R., Duggal P., Ginsburg G.S., Beggs A.H.;
"Multiple different missense mutations in the pore region of HERG in patients with long OT syndrome.";
                                                                                                                                                                                                                                                                                                                                                                 Keating M.T.;
"A molecular basis for cardiac arrhythmia: HERG mutations cause long QT syndrome.";
Cell 80:795-803(1995).
VARIANT LQT2 MET-822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT LQTZ ARG-593.
WEDLINE-96259954; PubMed-8635257;
WEDLINE-96259954; PubMed-8635257;
WEDLINE-96259954; PubMed-8635257;
Sendman C.E., Satler C.A., Vesely M.R., Walsh E.P., Sendman J.G., Sendman C.E., Satler C.A.;
"Missense mutation in the pore region of HERG causes familial long (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Novel missense mutation in the cyclic nucleotide-binding domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97071892; PubMed-8914737;
Satler C.A., Walsh E.P., Vesely M.R., Plummer M.H., Ginsburg G.S.,
                                                                                                                                                            T., Nakayama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic structure of three long QT syndrome genes: KVLQT1, HERG,
                                                                                                                                                                                                                                                                                 identification of a novel inherited mutation associated with long
                                                                                                                                                                                                                                                                                                                                                        Curran M.E., Splawski I., Timothy K.W., Vincent G.M., Green E.D.,
                                                                                                                                                                                                                                                                                                                                 SER-628 AND 500-ILE--PHE-508 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS LOT2 CYS-572; ASB-588; VAL-614 AND ALA-630.
MEDLINE-98360095; PubMed-9693036;
Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,
Keating M.T.;
                                                                                                                                                        Itoh T., Tanaka T., Nagai R., Kamiya T., Sawayama T., Nakayama Tomnike H., Sakurada H., Yazaki Y., Nakamura Y.; "Genomic organization and mutational analysis of HERG, a gene responsible for familial long QT syndrome."; Hum. Genet. 102:435-439(1998).
                                                                                                                                                                                                                                            Paulussen A., Verhasselt P., Crabbe R., Luyten W.,
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       Armstrong M.; **Analysis of the human HERG gene: intron localisation and
                                                                                                                                                                                                                                                                                                        Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).
                                                                                                                                 SEQUENCE FROM N.A., AND VARIANT LQT2 CYS-534.
MEDLINE-98260867; PubMed-9600240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G causes long QT syndrome.";
J. Med. Genet. 65:27-35(1996).
                                                                                                                                                                                                                                                                                                                                           MEDLINE=95196272; PubMed=7889573;
                                                                                                                                                                                                                                                                                                                                 VARIANTS LQT2 ASP-470; VAL-561;
                                                                                                                                                                                                                      (3)
SEQUENCE OF 27-1159 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circulation 95:565-567(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 51:86-97(1998).
                                                TISSUE-Hippocampus;
                                    SEQUENCE FROM N.A.
             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacob H.J.
                                                                                                mammals
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MIRPI ARE MORE STABLE.

-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.
-2- LUSSUES SPECIFICITY: HIGHLY EXPRESSED IN HEART.
-3- LOFEGES: DEFECTS IN KCH4Z IS ASSOCIATED WITH LONG OT SYNDROME TYPE
-2 (LOT2). THIS DISEASE IS CHARACTERIZED BY A PROLONGED OT SEGMENT ON THE ECG AND POLYMORPHIC VENTRICULAR ARRHYTHMIAS KNOWN AS TORARDES DE POINTESS. THESES ARRHYTHMIAS OFFERD OCCUR IN RELATION TO EXERCICE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT SYNCOPE, SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFFEN ASSOCIATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT LQTZ LYS-629.
MEDLINE=99445248; PubMed=10517660;
Yoshida H., Horie M., Otani H., Takano M., Tsuji K., Kubota T.,
Fukunami M., Sasayama S.;
"Characterization of a novel missense mutation in the pore of HERG in
a patient with long QT syndrome.";
J. Cardiovasc. Electrophysiol. 10:1262-1270(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Spectrum of mutations in long-QT syndrome genes. KVLQT1, HERG, SCN5A, KCNE1, and KCNE2.";
Circulation 102:1178-1185(2000).
                                                                                                                                                                                                                                                                                                                                                            VARIANTS LOT2 PRO-558; CYS-582; SER-604; MET-613 AND LEU-640. MEDLINE-9232550; Dubade-1022014; MEDLINE-9232550; Dubade-1022014; Jondbloed R.J.E., Wilde A.A.M., Gelen J.L.M.C., Doevendans P., Schaap C., Van Langen I., Van Tintelen J.P., Cobben J.M., Beaulort-Krol G.C.M., Geraedts J.P.M., Smeets H.J.M.; "Novel KCNQ1 and HERS missense mutations in Dutch long-QT families."; Hum. Mutat. 13:301-310(1999).
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MEDILDE-20197880; Pubmed-10735633;
Larsen L.A., Svendsen I.H., Jensen A.M., Kanters J.K., Andersen P.S.,
Moller M., Sorensen S.A., Sandoe E., Jacobsen J.R., Vuust J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS LQT2 L-29; T-33; R-53; Q-56; G-66; R-70; P-78 AND R-86. MEDLINE-99214568; PubMed-10187793; Chen J., Zou A., Splawski I., Keating M.T., Sanguinetti M.C.; "Long QT syndrome-associated mutations in the Per-Arnt-Sim (PAS) domain of HERG potassium channels accelerate channel deactivation."; J. Biol. Chem. 274:10113-10118(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Long QT syndrome with a high mortality rate caused by a novel G572R missense mutation in KCNH2.";
Clin. Genet. 57:125-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: IT HAS THE ARCHITECTURAL PLAN OF THE DEPOLARIZATION-ACTIVATED POTASSIUM CHANNEL FAMILY (6 PUTATIVE TRANSMEMBRANE SECHENTS), YET IT EMILITS RECTIFICATION LIKE THAT OF THE INWARD-RECTIFING POTASSIUM CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=20432616; PubMed=10973849;
Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori S.,
Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,
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- SUBUNIT: MAY ASSEMBLE WITH EITHER MIRPI OR MINK, COMPLEXES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99235552; PubMed-10220146;
Larsen L.A., Christiansen M., Vuust J., Andersen P.S.;
Wigh-throughput single-strand conformation polymorphism analysis bautomated capillary electrophoresis: robust multiplex analysis and pattern-based identification of albelic variants.";
Hum. Mutat. 13:318-327(1999).
                                      MEDLINE-98112459; PubMed-9452080;
Akinato K., Furutani M., Imamura S.-I., Furutani Y., Kasanuki H.,
Takao A., Momma K., Matsuoka R.;
"Novel missense mutation (G601S) of HERG in a Japanese long QT
                                                                                                                                                                                                                                                                      Hum. Mutat. Suppl. 1:S184-S186(1998)
VARIANTS LOT2 SER-601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT LQT2 ARG-572.
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                                                                                                                                                                                                                                                                                                                                                                                    Zhao J.J., Lazzarini R.A., Pick L.;
"Functional dissection of the mouse Hox-a5 gene.";
EMBO J. 15:1313-1322(1996).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTIFIES ON THE ANTERIOR-POSTERIOR AXIS.
ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-CYYNATTA[TG]Y-3'.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                      "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                       "Coding sequence and expression of the homeobox gene Hox 1.3."; Development 102:349-359(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                 Tani M., Lazzarini R.A.;
"Expression of a homeo domain protein in noncontact-inhibited
                                                                                                                                                                                                                                                             MEDLINE-89232713; PubMed=2565857;
Odenwald W.F., Garbern J.; Arnheiter H., Tournier-Lasserve E.
                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-8832807; PubMed=2901335;
Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labeit S.,
Lehrach H., Gruss P.;
                                       SEQUENCE FROM N.A.
MEDLINE-88056292; PubMed-2890554;
Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V.
Tani M., Lazzarini R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTP-TYPE HEXAPEPTIDE
                                                                                                            cultured cells and postmitotic neurons."; Genes Dev. 1:482-496(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 85;
                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE-96205869; Pubmed-8635464;
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PRINTS; PR00025; ANTENNAPEDIA.
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DNA-BINDING SPECIFICITY.
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InterPro; IPR001356; -
InterPro; IPR001827; -
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TRANSFAC; T00377; -
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               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                         Lazzarini R.A.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 85.5; DB 1; Length 1159; 26.6%; Pred. No. 23; tive 10; Mismatches 51; Indels 55
DATABASE: NAME-LQTSdb; NOTE-KCNH2 mutations page;
WWW-"http://www.ssi.dk/en/forskning/lqtsdb/herg.htm".
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01.NOV-1988 (Rel. 09, Last sequence update)
01.0CT-1996 (Rel. 34, Last annotation update)
HOMEOBOX PROTEIN HOX.A5 (HOX-1.3) (M2).
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Matches 42; Conservative
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AJ010551;
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ID HXA5_MOUSE
AC P09021;
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                                                                                                                                                                                                                                                                                                    86 YSQPATSTHSPPDPLPCSAVAPSPGSDSHHGGKNSLGNSSGASANAGSTHISSREGVGT 145
                                                                                                                                                                                                                                                                                                                                                                        73 ----HSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEFVDSFKKG 128
                                                                                                                                                                                                                                                                                                                                                                                                                  72 SAHHGAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHW 131
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                                                Gaps
                                                                                                                                                   10 SEQ-EDSSSAERG-----LGPSPAGDGPSGSGKHHRQ-----APGLLWDASHQ 51
                                                                                                                                                                                                                                         -----SHHGG------72
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"E3, a hematopoietic-specific transcript directly regulated by the retinoic acid receptor alpha.";
Blood 88:2517-2530(1996).
-:- TISSUE SPECIFICITY: PRESENT IN THE MYELOID, B-LYMPHOID, AND ERYTHROID LINEAGES, ABSENT IN NONHEMATOPOIETIC CELLS.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RETINOIC ACID-INDUCIBLE E3 PROTEIN (HEMATOPOIETIC-SPECIFIC PROTEIN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                82;
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+ive 13; Mismatches
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MEDLINE-96437028; PubMed-8839844;
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09eru8 mus musculu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Ottilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,
Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;
J. Biol. Chem. 0:0-0(1997).
EMBL; AF021792; AAB72032.1; -.
EMBL; AF031523; AAB88124.1; -.
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MEDLINE=97083574; PubMed=8929532;
MEDLINE=97083574; Rapp U.R., Reed J.C.;
"Bcl.-2 targets the protein kinase Raf-1 to mitochondria.";
cell 87:629-638(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Takayama S., Reed J.C.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;
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 Homo sapiens (Human).
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091837 homo sapien
096789 herpesvirus
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09618 streptomyce
09188 homo sapien
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Copyright (c) 1993 - 2000 Compugen Ltd.
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MEDLINE-98194755; PubMed-9535132;
D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
"Clôning and expression of the programmed cell death regulator Bad in
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hsu S.Y., Hsueh A.J.W.;
"Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced apoptoois in mammalian cells by 14-3-3 isoforms and Pll.";
Mol. Endocrinol. 11:1858-1867(1997).
EMBL; AF003523; AAC53374.1;
SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;
HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                 61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRRSDE 120
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                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQE-QPTSSS 59
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_PaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 MFQIPEFEPSEQEDASTIDRGLGPSLIEDQP---GPY--LAPGLLGSIVQQQPGQAANNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.0%; Score 633.5; DB 11; Length 205; Best Local Similarity 74.6%; Pred. No. 2.3e-50; Matches 126; Conservative 12; Mismatches 24; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                   121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                    (TremBLrel. 05, Created)
(TremBLrel. 05, Last sequence update)
(TremBLrel. 08, Last annotation update)
                                                                                                                                                                                      205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. Lett. 243:137-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98034386; PubMed=9369453;
                                                                                                                                                                                                                                                                     BCL-2 ASSOCIATED DEATH PROMOTER. BAD.
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98 HHGGAGTWETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSD 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 HHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMAD 119
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SEQUENCE FROM N.A.

Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;

"Functional characterization of two splice variants of rat bad and
their interaction with bcl-w in sympathetic neurons.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF03127; AAC15100.1;

EMBL; AF279910; AAF91427.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
"Functional characterization of two splice variants of rat bad and their interaction with bcl-w in sympathetic neurons.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
BENBL; ARZ79911; AAF914281; -
SEQUENCE 220 AA; 24278 MW; E27BCCD7C969E90F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQE-QPTSSS 59
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9
                                                                                                                                                                                                                                                                                                                Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 EFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
BCL-2 ASSOCIATED DEATH AGONIST BETA.
                                                                                                                                                                                                                                                                                                                   70.0%; Score 633.5; DB 11; 74.6%; Pred. No. 2.3e-50;
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                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
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STRAIN-BABDOON LYMPHOCRYPTOVIRUS BA65;

Long J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,

Hayward G.S.;
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MEDLINE=20501263; Pubmed=11046149;
Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;
Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;
"Characterization of dfwhl, a Drosophila melanogaster Homolog of the Fragile X Mental Retardation Protein.";
Mol. Cell. Biol. 20:8536-8547(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG----GA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 EQEDSSSAERGLGPSPAGDGPSGSGKHHRQAP----GLLWDASHQQEQPTSSSHHGGAGA 66
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KH DOMAIN CONTAINING TANA-BINDING PROTEIN FMR1.
Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Arabish) (Zebra danio).
Actinopterygii; Neopterygii; Teleosatei; Euteleostomi; Actinopterygii; Neopterygii; Seleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 100; DB 14; Length 608; 33.3%; Pred. No. 0.27; tive 7; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF200364; AAF23950.1; --
SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   569 AA; 63906 MW; 2E66A0689F7EDFB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpesvirus papio.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                           608 AA
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                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                           PRT;
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       127 KGLPRPKSAGTATQMRQSSSWTR 149
                                                                  193 TGLARLLSRLSGVGLRLTTSLFR
                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 20:8536-854
EMBL; AF305882; AAG22046.1;
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Best Local Similarity 33.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Conservative
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                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSSDSGSAEKRRKSPGGGGGGGGGGGGGNDNNQA------ATKSPRKAAAAARL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RSRHSSYPAGTEDD-EGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRR-MADEFVDSFK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20373792; PubMed=10917738;
Inohara N., Nunez G.;
"Genes with Homology to Mammalian Apoptosis Regulators Identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu R., Misra V.; "Zhangfei: a second cellular protein interacts with herpes simplex virus accessory factor HCF in a manner similar to Luman and VP16."; Nucleic Acids Res. 28:2446-2454(2000).
EMBL, AF039942; AAD28325.1; -.
InterPro; IPR001871; -.
                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii: Neopterygii; Teleostei: Euteleostei; Ostariophysi;
Cypriniformes: Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.6%; Score 204.5; DB 13; Length 95; 48.9%; Pred. No. 1.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.0%; Score 100; DB 4; Length 272; Best Local Similarity 28.7%; Pred. No. 0.12; Matches 41; Conservative 13; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28859 MW; B1F94B438F0702BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-MAR-2001 (TrEMBLrel. 16, Last annotatio
HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 TOMROSSSWIRVFOSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROMSOSPSWLAFL --- WSHKESDAESRPAE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell Death Differ. 7:509-510(2000).
EMBL; AF231017; AAF66962.1; ...
NON TER 1
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MEDLINE=20330366; PubMed=10871379;
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SMART; SM00338; BRLZ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                      BAD (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebrafish.";
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SEOUENCE
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Q9NS37
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Gaps

12;

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Gaps

15;

Indels

42;

Length 569;

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Gaps

28;

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Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).

EMBL: AL136518; CAB66246.1;
InterPro; IPR000445;
InterPro; IPR00633; HHH; 1.

Pfam; PF00633; HHH; 1.

SMART: SM00278; HHH; 1.

SMART: SM00278; HHH; 1.

SMART: SM00278; HHH; 1.

SMART: A10678; HHH; 1.

SMART: A10678; HHH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 -----OPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 -HSSYPAGTEDDEGMGEEPSPFRGRSRSAP - - PNLWAAQRYGRELRRMADEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPOWERE;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Hsiao J., Ziamann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
Bueman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBD0073A24 genomic sequence.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC078840; AAG136311; -
SEQUENCE 867 AA; 94083 MW; 4FEA69E1BFCOCB2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 SSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHG--GAGAVEIRSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 EDSSSAERGLGPSPAG----DGPSGSGKHHRQAP-----GLLWDASHQQE---
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                                                                                                                                                                                                                                                                                                                                                                                    Length 355,
                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AETLFAERAEGYDHAGHEGA--HGETGKGPPLPGLDAPARQGSPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 10.8%; Score 98; DB 2; 28.5%; Pred. No. 0.23; iive 14; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 PRPKSAGTATQMRQSSSWTRVFQSWWDRNLG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 DAPTGPGTAWRERAGSALRERMPLWLQTRCG 136
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01-MAR-2001 (TrEMBLrel. 16, Le
PUTATIVE REPLICATION PROTEIN.
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Best Local Similarity 28.5%
Matches 43; Conservative
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836 RREERRLGR 844
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Q9FV26;
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Q9FVZ6
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     846 SNSHNGVQAAA---SGTGRMSAANSGRVGNGSVPP----RNGRRRAPLAEAILDTLTA 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEI 69
                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005941, AaF34290.1; -.
InterPro; IPRO01931; -.
PRINTS; PR00194; TROCMYOSIN.
SEQUENCE 923 AA; 103964 MW; C229C15F6448F7C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
MEDLINE-97000351; Pubmed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.9%; Score 98.5; DB 5; Length 923; Best Local Similarity 27.2%; Pred. No. 0.56; Matches 34; Conservative 20; Mismatches 44; Indels 2
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
         Created)
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Thomson N.R., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Brown S.P., Harris D.;
Submitted (JAN-2000) to
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=FRIEDLIN;
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897 GPPQP 901
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09RDL8
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2335 TSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPGPARSESPRACRHGGARWPASG 2394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20219126; PubMed=10753886; Toru S., Murakoshi T., Ishikawa K., Saegusa H., Fujigasaki H., Uchihara T., Nagayama S., Osanai M., Mizusawa H., Tanabe T.: Spinocerebellar ataxia type 6 mutation alters P-type calcium channel
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                         15 SSSAERGLGPSP---AGDGPSGSGKHHRQAP------GLLWDAS- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                         50 -HQQEQPTSSSHHGGAGAVEIRSRHSSYPAGTEDDE-----GMGEE------PSPFR 94
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    :69
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                                                                                                                                                                                                                                                                             4; Length 2506;
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                                                                                                                                                                                                                                                                                                                  50; Indels
                                                                                                                                                                                                                     D64A6C75284A1B53 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 16, Last annotation update)
ALPHAIA-VOLTAGE-DEPENDENT CALCIUM CHANNEL (FRAGMENT)
                                                                                                                                                                                                                                                                           10.7%; Score 96.5; DB 25.1%; Pred. No. 2.4; ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2472 AA
                      275:10893-10898(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function.";
J. Biol. Chem. 275:10893-10898(2000)
EMBL, 8035726; BAA94765.1; -.
InterPro; IPR00063g; -.
                                                                                                                                                      Pfam; PF00520; ion_trans; 4. PRINTS; PR00167; CACHANNEL. SMART; SMO0384; AT_hook; 1. SEQUENCE 2506 AA; 282580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278845 MW;
  function.";
J. Biol. Chem. 275:10893-108
EMBL; AB035727; BAA94766.2;
InterPro; IPR000636; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00384; AT_hook; 1.
NON_TER 2472 2472
                                                                                                                                                                                                                                                                           Query Match 10.79
Best Local Similarity 25.19
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                InterPro; IPR001682; -. InterPro; IPR002077; -.
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                                                                                                                                         InterPro: IPR002111; -
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2472 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GRS----RSAPPNLWAAQRYGRELRRMADEFVDSFKKGLPRPKSAGTATQMRQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20219126; PubMed-10753886;
Toru S., Murakoshi T., Ishikawa K., Saegusa H., Fujigasaki H.,
Uchihara T., Nagayama S., Osanai M., Mizusawa H., Tanabe T.;
"Spinocerebellar ataxia type 6 mutation alters P-type calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Gaps
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                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Black J.L., Snutch T.P., Lennon V.A.;
Partial sequence of Homo sapiens P/Q-type voltage-gated calcium channel alpha 1 (alpha 1A) subunit isolated from small cell lung carcinoma cell line, SCC 9, CDNA library.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF100774; AAC77460.1;
InterPro; IPR000635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 980;
                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
VOLTAGE-DEPENDENT P/Q TYPE CALCIUM CHANNEL ALPHA 1A SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ALPHAIA-VOLTAGE-DEPENDENT CALCIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 96.5; DB 25.1%; Pred. No. 0.91; vative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 SSSAERGLGPSP---AGDGPSGSGKHHRQAP----
                                         980 AA.
                                         PRT;
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PRINTS; PR00167; CACHANNEL.
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Best Local Similarity 25.1%
Matches 46; Conservative
                                         PRELIMINARY;
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                                                                                                                                                        (FRAGMENT).
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                                                         395387;
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                                       095387
RESULT 12
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                                                                                                                                              2215 HHHHHPPPPDDKDRYAQERPDHGRARARD---QRWSRSPSEGRE--HMAHRQGSSSVSGS 2269
                           1235 HHLQQQRMAMMSQPQPQAFSPPNVTASPSMDGVLAGSAMPQAPPQQFPYPA----NYG 1290
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Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K., Rosenfeld M.G.;
"The transcriptional co-activator p/CIP binds CBP and mediates nouclear-receptor function.";
Nature 387:677-684(1997).
                                                                                                          71 SRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWA-AQRYGRELRRMADEFVDSFKKGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 MGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEFVDSFKKGLPRPKSAGTATQMRQSS 145
16 SSAERGLG-----PSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 HHRQAPGLLWDASHQQEQ------PTSSSHHGGAGAVEIRSRHSSYPAGTEDDEG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                              009000;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NUCLEAR RECEPTOR COACTIVATOR 3 (P300/CBP/CO-INTEGRATOR PROTEIN).
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Pfam; PF00989; PAS; 1.
SMART; SM00091; PAS; 1.
SEQUENCE 1398 AA: 151573 MW; EF44E92735816C24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Torchia J., Rosenfeld M.G.;
Submitted (MAR.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFG005913 aAC0502020.1;
MGD; MGI:1276535; Nooa3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Torchia J., Rosenfeld M.G.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      2270 PAPSTSGTSTSRGRRQLPQTPSTPRPHVSYSPVIRKAGGSGPPQ 2314
                                                                                                                                                                                                                    130 PRPKSAGTAT-----QMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.4%; Score 94.5; DB 11; Best Local Similarity 25.9%; Pred. No. 2; Matches 37; Conservative 12; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Search completed: October 9, 2001, 16:03:21 Job time: 306 sec 09-580523-1b.rag

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Shorter murine BAD
bcl-x(L)/bcl-2 ass
Murine BCL-XL/BCL-
Murine BAD protein
Longer murine BAD
Mutant BCL-XL/BCL-
                                                                                                                                                                                                        (without alignments)
305.943 Million cell updates/sec
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Human cell prolife
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1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ 168
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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AAW58832
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AAW32476
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Gapop 10.0 , Gapext 0.5
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### ALIGNMENTS

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Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease
                                                                                                  Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad; programmed cell death; apoptosis.
                                                                               Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
                    AAW55779 standard; Protein; 168 AA
                                                                                                                                                                                                         96US-0717123.
                                                                                                                                                                                           97WO-US16991.
                                                          (first entry)
                                                                                                                                                                                                                                                      Horne WA, Oltersdorf T;
                                                                                                                                                                                                                                  (IDUN-) IDUN PHARM INC.
                                                                                                                                                                                                                                                                        WPI; 1998-217267/19.
N-PSDB; AAV25877.
                                                                                                                                                   WO9812328-A2.
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                          18-SEP-1997;
                                                                                                                                                                                                             20-SEP-1996;
                                                          17-JUL-1998
                                                                                                                                                                       26-MAR-1998
                                     AAW55779;
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RESULT
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Claim 8; Fig 1; 41pp; English

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            The present sequence is the human Bcl-xL/Bcl-2 associated death promoting polypeptide, Bad, the binding of which to Bcl-Xl results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as conscious characterised by apoptotic cell death, such as characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa and cerebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to treat or prevent diseases characterised by the loss of apoptotic cell death, such as cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide and polypeptide sequences of proteins associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cell proliferation; APOP-1; cancer; inflammation; infection; trauma; neurodegenerative disease; ischaemic injury; wasting disease.
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                                                                                                                                                                                                                                          diseases, e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis and viral infections, e.g. herpesvirus, poxvirus or adenovirus infection. Bad can also be used for
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                                                                                                                                                                                                                                                                                                                                                                                      Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                  Score 902; DB 19;
Pred. No. 7.2e-88;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cell proliferation protein APOP-1.
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99.4%;
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                                                                                                                                                                                                                                                                                                  detection and diagnosis
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Best Local Similarity
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The present sequence is the human APOP-1 protein. This protein, which shares structural and chemical homology with Bcl-2, is involved in cell proliferation. Its coding sequence was isolated by screening a synovial tissue cDNA library using a computer search for amino acid sequence alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated inflammation such as Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus, cmphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, rhemmatoid arvitis, sygren's syndrome and autoimmune thyroiditis, complications of cancer, haemodialysis and extracorporeal circulation, infections, trauma, disorders with associated apoptosis including AIDS and other infectious and genetic immunodeficiencies, meurodegenerative diseases such as Alzheimer's diseases and parkinson's diseases including cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó,
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Pred. No. 7.2e-88;
1; Mismatches 0;
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Example 8; Fig 1; 58pp; English.
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Best Local Similarity
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\overset{\mathsf{A}}{\times}\overset{\mathsf{X}}{\times}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{O}}{\circ}\overset{\mathsf{
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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WPI; 2001-138734/14.

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AAB48287 standard; protein; 168 AA. Claim 1; Page 147; 157pp; English. 02-APR-2001 (first entry) Matches 167; Conservative Similarity 168 AA; Human Bad protein. WO200075184-A1. Homo sapiens mutant apoptosis, AAB48287; Sequence Query Match Best Local useful Ser113 61 AAB48287 RESULT οy à q ŏ 윱 셤

The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin, CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c.Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168 Score 902; DB 22; Pred. No. 7.2e-88; BBC6 gene; cell death; cell cycle; Bcl2; human. 1; Mismatches BBC6 protein for regulating cell death. Claim 5; Page 102-103; 162pp; English. AAW32476 standard; Protein; 166 AA, Kondo T; 99.7%; 96US-0665617 96US-0665617 (first entry) Matches 167; Conservative (CLON-) CLONTECH LAB INC. Tsvetkov LM, WPI; 2001-061703/07. N-PSDB; AAC84599. Similarity 168 AA; Homo sapiens, 18-JUN-1996; 18-JUN-1996; 15-JAN-1998 US5663316-A. 02-SEP-1997 Zhang H, Seguence Xudong Y; AAW32476; Query Match Best Local S AAW32476 RESULT οy 셤 g δ The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

(I) comprising a less than full length amino acid sequence of a mutant

(I) associated cell death requiator polypeptide (BAD) or its

(I) as immunostitutions at Seril3 of a human

(I) as immunostitution at Seril3 of a human

(I) has immunostitulant, antine

(I) as immunostition, antiviral, antine

(I) antiarthritic, antiliflammatory and immunosuppressive activities, and

(I) antiarthritic, antiliflammatory and immunosuppressive activities and

(I) antiarthritic, antiliflammatory and immunosuppressive activities and

(I) antiarthritic, antiliflammatory and immunosuppressive activities and

(I) antilified and (I) appreciate and a call activity and antilified and (I) antiarthritis, and a call anti-infections, arthritis, infertility, inflammation and

(I) autoimmune diseases. The present sequence represents a specifically

(I) antiarthritic.

(I) antiarthritis, antility, inferting antipon. ö 61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120 S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic. Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, screening for candidate compounds which induce or inhibit comprises amino acid substitutions at Serl18, Serl55 or Gaps 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60 ö Length 168; 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168 Indels Score 902; DB 22; Pred. No. 7.2e-88; 1; Mismatches 0; 99.7%;

Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bcl-2

WPI; 1997-447980/41.

05-JUN-2000; 2000WO-US15449.

14-DEC-2000

99US-0137494

04-JUN-1999;

(UYYA ) UNIV YALE.

N-PSDB; AAT91561.

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Gaps

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Indels

Length 168;

9

Tue Oct

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The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with Bcl-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease; neurodegenerative disease; viral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                               54 QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 qptssshhggagaveirsrhssypagteddegmgeepspfrgararpppnlwaagrygre 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
                                                                                                                                                                                                                                                                                                                                          1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPG-----LLWDASHQQE 53
                                                                                                                                                                                                                                                                                                                                                                           1 mfqipefepseqedsssaerg-wrspagtgp-----qapasiiarpqvlwdashqqe 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 LRRMADEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                   Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                  Score 748; DB 18;
Pred. No. 1.5e-71;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 148-149; 157pp; English.
                Claim 1; Column 11-12; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB70370 standard; protein; 162
                                                                                                                                                                                                                                                                  82.7%;
ilarity 83.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0136783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000WO-US11864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                 Æ
                                                                                                                                                                                                                 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB70370;
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ser113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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The present invention describes an isolated or synthetic polypeptide

(I) comprising a less than full length amino acid sequence of a mutant

Bel-XL/Bel-2 associated cell death regulator polypeptide (BAD) or its
fragment, which contains anno acid substitutions at Seril8 of a human

E BAD, Seri55 of a mutine BAD) or Seril8 of a mutine

C and chorter mutine BAD). (I) has immunostimulant, neuroprotective,
nootropic, antiischaemic, vinnerary, cytostatic, antiviral,
can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
cor necessary and immunosuppressive activities, and
cor activity that promote cell survival or apoptosis. Other uses include
inducing or inhibiting apoptosis in a cell. Candidate compounds
conducting and (mutant) BAD polypeptides are useful in treating
immunodeficiency diseases, neurodegenerative diseases, ischnemic cell
cdeath, reperfusion cell death, wound healing, cancer, viral infections,
lymphoproliferative conditions, arthritis, infertility, infammation and
claimed shorter murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "BH1 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "BH2 conserved amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bcl-x(L)/bcl-2 associated death promoter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 646; DB 2;
Pred. No. 9e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111..130
/note= "PEST sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "PEST sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR95168 standard; Protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                   71:4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..192
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               162 AA;
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Qγ
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18-OCT-1996;
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                                                                                                                                                                              This sequence represents the murine bcl-x(L)/bcl-2 associated death bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2 related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), and its also conners the accelerate apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line expressing bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L) corn heterodimers. Such agents may be used to treat neurodegenerative diseases, immunodeficiency diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine BCL-XL/BCL-2 associated cell death regulator.
                                                                                                                                                                                                                                                                                                                                                senescence or ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW61315 standard; Protein; 204
                                                                                                                                                            Claim 3; Fig 1; 130pp; English
         94US-0333565.
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                                (UNIW ) UNIV WASHINGTON.
                                                                             WPI; 1996-251465/25.
N-PSDB; AAT29479.
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                    204 AA;
                                                       Korsmeyer SJ;
         31-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Sim
Matches 126;
                                                                                                                                                                                                                                                                                                                                                                       Seguence
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence is the murine BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD protein able to decrease cell viability; (2) increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, confirmation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers or creament of excessive apoptosis such as AIDS, neurodegeneration, adjug or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, we usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family contents in the cytosol, thus promoting cell survival. The mutants with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                Claim 1; Fig 10; 95pp; English.
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WPI; 1998-261422/23.
N-PSDB; AAV27833.
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Matches 126;
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                                                                                                                                                                                                                                                                                                                             (BC1-X1/BC12 associated cell death regulator). The serine residue is phosporylated in a post-translational modification and allows binding to the 14-3-3 protein which is a signal transduction regulator.

Modulators of phosphorylated BAD, which act through inhibition/activation of a phosphoserine phosphatase, are useful for preventing/treating increased/decreased apoptosis in a cell. The increased apoptosis may result from immunodeficiency diseases, senescence, neurodegenerative wound-healing. Decreased apoptosis may result from cancer, viral inferting Decreased apoptosis may result from cancer, viral inflammation and autoimmune diseases. Measuring the amount of phosphorylated autoimmune diseases. Measuring the amount of phosphorylated compared to unphosphorylated BAD polypeptide and/or total BAD in a cell is useful for determining the apoptotic state of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 hggagametrsrhssypagteedegmeeelspfrgrsrsappnlwaagrygrelrrmsde 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine-phosphorylated Bcl-X-1/Bcl-2 Associated cell Death regulator polypeptide - useful for modulation of apoptosis associated with, e.g. cancer and immunodeficiency diseases
                                                                                                                                                                                                                                                                                                                     This sequence represents a novel serine-phosphorylated protein, BAD
cancer, viral infection; lymphoproliferative condition; arthritis; inflammation; autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 646; DB 19; 75.0%; Pred. No. 1.2e-60; iive 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB70369 standard; protein; 204 AA
                                                                                                                                                                                                                                                                                            Claim 3; Fig 8; 61pp; English.
                                                                                                                                       96us-0707868.
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Matches 126; Conservative
                                                                                                                                                                (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                 WPI; 1998-207049/18.
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                                                                                                                                                                                          Korsmeyer SJ;
                                                            WO9809643-A1
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                                                                                     12-MAR-1998
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for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, murodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, authorities, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically claimed longer murine BAD mutant amino acid sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser118 of a human BAD, Ser155 of a mutine BAD (longer mutine BAD) or Ser113 of a mutine BAD (shorter mutine BAD). (1) has immunostimulant, neuroprotective, nootropic, antiinflammatory and immunosuperssive activities, and antiatritic, antiinflammatory and immunosuperssive activities, and pell sinducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs.
immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunodeficiency disease, neurodegenerative disease, urral infection; ischaemic cell death; reperfusion cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000; 2000WO-US11864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
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Viral infection, 19mpDoroliferation, arthritis, infertility, untaint and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and nongreater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heteroding activity than instead blinds to 14.3-3 family hard and the circular and the content of the conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer,
                                                                                                                                                                                        Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                          Mutant BCL-XL/BCL-2 associated cell death regulator #2.
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AAW61317;
                                                                                                                                                                                                                                                                                        Mus
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3; Gaps 1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60 .. 9 71.0%; Score 643; DB 19; Length 204; 74.4%; Pred. No. 2.5e-60; Ative 14; Mismatches 23; Indels ( Best Local Similarity 74.49 Matches 125; Conservative Query Match õ g

61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120 

ŏ g 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168 ò

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Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
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Mutant BCL-XL/BCL-2 associated cell death regulator #1.
                                                                                                                                                                                         AA.
                                                                                                                                                                                  AAW61316 standard; Protein; 204
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Synthetic.
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat corprevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, infertility, infilammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as Albs, neurodegeneration, aging or ischemic cell death. The apoptotic status of cells is the phosphorylated and non-phosphorylated phosphorylated made by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

Claim 7; Page 59; 95pp; English.

204 AA; Sequence

Gaps ; 9 70.7%; Score 640; DB 19; Length 204; 73.8%; Pred. No. 5.2e-60; Indels 15; Mismatches Matches 124; Conservative Best Local Similarity Query Match

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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60

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09-580523-1b.rag

204 AA;

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CC viral infection, lymphoproliferation, arthritis, infertility.

CC mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is concernined by measuring relative amounts of phosphorylated and non-phosphorylated on the specified Ser, forming a product that does not phosphorylated on the specified Ser, forming a product that does not phosphorylated on the specified Ser, forming a product that does not peterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL-XL/BCL-2 associated cell death regulator; BAD protein;
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                                                                                                      98 hggagametrsrhsaypagteedegmeeelspfrgrsraappnlwaagrygrelrrmsde 157
HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                    121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                     Mutant BCL-XL/BCL-2 associated cell death regulator #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 60-61; 95pp; English.
                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                            AAW61318 standard; Protein; 204
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N-PSDB; AAV27836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
                                                                                                                                                                                                                                                                        61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAORYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                       98 hggagametrsrhsaypagteedegmeeelspfrgrsraappnlwaagrygrelrrmsde 157
                                                                         Gaps
                                                                                                                                                                              in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is
                                                                                                                                       1 MFQIPEFEPSEOEDSSSAERGLGPSPAGDGPSGSGKHHROAPGLLWDASHOOEOPTSSSH
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      Length 204;
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;; Score 640; DB 19;
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15; Mismatches 23;
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   70.7%;
73.8%;
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      Query Match
Best Local Similarity
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determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14 3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14 3-3.

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Gaps

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Length 59; indels

Score 311; DB 19; Pred. No. 7.7e-26; 1; Mismatches

34.48; 98.38;

Best Local Similarity 98.3 Matches 58; Conservative

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Gaps

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Length 59; Indels

Query Match

59 AA;

Sequence

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phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.
                                                                                                                                                       GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEF 121
 determined by measuring relative amounts of phosphorylated and non-
                                                                                                                                                                Mutant BCL-XL/BCL-2 associated cell death regulator #5.
                                                                                                              Score 311; DB 19;
Pred. No. 7.7e-26;
1; Mismatches 0;
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                                                                                                             Query Match 34.4%;
Best Local Similarity 98.3%;
Matches 58; Conservative
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                                                                               59 AA;
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63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEF 121 Search completed: October 9, 2001, 15:59:14 Job time: 99 sec ò g death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein Also described are: (1) fusion proteins of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, entrritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection. The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell 59 New mutant BAD polypeptide with phosphorylatable serine replaced useful for, e.g. treating reduced apoptosis such as in cancer or viral infection Claim 8; Page 73; 95pp; English.

Appli

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Scoring table:

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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APOPPOSIS TECHNOLOGY, INC.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,

TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS

TITLE OF INVENTION: THAT REGULATE APOPTOSIS

FILE REPERRNCE: F137122

CURRENT APPLICATION NUMBER: PCT/USO0/11864

CURRENT FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 1
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99.4%; Pred. No. 7.4e-71;
ive 1; Mismatches 0; Indels
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PCT-US00-11864-3

US-09-580-523-3

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US-08-707-868-41

US-08-707-868-41

US-08-707-868-41

US-08-707-868-41

US-09-375-257-3

US-09-375-257-3

US-09-375-257-3

US-09-375-257-3

US-08-733-505-14

PCT-US97-15871A-12

PCT-US97-15871A-12

PCT-US97-15871A-12

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US-09-656-399-15
US-09-656-399-16
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS0011864 GENERAL INFORMATION:
                                           Query Match 99.7
Best Local Similarity 99.4
Matches 167; Conservative
   ORGANISM: Homo sapiens
PCT-US00-11864-1
   RESULT 1
PCT-US00-11864-1
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1 MFQIPEFEPSEQEDSSSAER.....RVFQSWWDRNLGRGSSAPSQ 168
                                                                      Search time 164.17 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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7 US-09-375-257-2

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Result SO. 09-580523-1b.rapm

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121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                                          Sequence 1, Application US/09410372
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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Best Local Similarity 99.4'
Matches 167; Conservative
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MEDIUM TYPE: Diskette
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US-09-410-372-1
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US-09-456-357-32
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Pred. No. 7.4e-71;
1; Mismatches 0; Indels
                                                                                                                                     APPLICANT: Oltersdorf, Tilman A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: ACIDS AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/375,257
CURRENT APPLICATION NUMBER: US/09/375,257
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENCODING NUCLEIC
FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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Pred. No. 7.4e-71;
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GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, F
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42802
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CURRENT FILIKG DATE: 1999-08-17
NUMBER OF ESO ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                       Sequence 2, Application US/09375257 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      99.78;
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Best Local Similarity 99.4%;
Matches 167; Conservative
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Best Local Similarity 99.4
Matches 167; Conservative
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CORGANISM: Homo sapiens
US-09-375-257-2
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LENGTH: 168
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LENGTH: 168
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
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121 FVDSFKKGLPRPKSACTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                             APPLICANT: Yue, Henry .
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROIFFRATION
TITLE OF INVENTION: PROLIFFRATION
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 902; DB 18;
Pred. No. 7.4e-71;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0421 US
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
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US-08-883-731-2
; Sequence 2, Application US/08883731
; GENERAL INFORMATION:
   APPLICANT: Zhu, Li
   APPLICANT: Xudong, Yin
   TITLE OF INVENTION: Gene and Protein for Regulation Cell Death
   FILE REFERENCE: D6120
   CURRENT APPLICATION NUMBER: US/08/883,731
; CURRENT APPLICATION NUMBER: US/08/883,731
; EARLIER APPLICATION NUMBER: US 08/665,617
; EARLIER FILING DATE: 1996-06-18
; NUMBER OF SEQ ID NOS: 3
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Pred. No. 7.4e-71;
1; Mismatches 0; Indels.
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                                                                    121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                                                                                        Sequence 21, Application US/09587473
GENERAL INFORMATION:
APPLICANT: Zhang, Hui
TITLE OF INVENTION: Protein Knockout Technology
FILE REFERENCE: 44574-5047-WO
CURRENT APPLICATION NUMBER: US/09/587,473
CURRENT APPLICATION NUMBER: US 60/137,494
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 21
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Best Local Similarity 99.4%;
Matches 167; Conservative 1
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US-09-587-473-21
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Matches 142; Conserva
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ORGANISM: unknown
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                                                                           TITLE OF INVENTION: WEAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND TITLE OF INVENTION: WETHORS FOR MAKING AND USING THE SAME FILE REFERENCE: 3921-1-1-1 CURRENT APPLICATION NUMBER: US/09/456,357 CURRENT FILING DATE: 1999-12-08 EARLIER FILING DATE: 1999-05-17 EARLIER APPLICATION NUMBER: 09/087,195 EARLIER APPLICATION NUMBER: 09/087,195 EARLIER APPLICATION NUMBER: 09/087,195 EARLIER PILING DATE: 1998-05-29 EARLIER FILING DATE: 1998-05-29 EARLIER FILING DATE: 1994-05-27 NUMBER: OF SEQ ID NOS: 50 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3: SEQ ID
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: A7483
FILE REFERENCE: A7483
CURRENT APPLICATION UNDHER: US/09/580,523
CURRENT FILLING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 7.4e-71;
1; Mismatches 0;
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Pred. No. 7.4e-71;
1; Mismatches 0;
Sequence 32, Application US/09456357 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09580523
GENERAL INFORMATION:
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Best Local Similarity 99.4<sup>1</sup>
Matches 167; Conservative
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Best Local Similarity 99.43
Matches 167; Conservative
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US-09-580-523-1
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                                                HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
WUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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Pred. No. 9.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTEM: DOS
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILLING DATE:
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APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                                                                                                                             Sequence 7, Application US/09410372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.5%;
Matches 142; Conservative
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amino acid
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MEDIUM TYPE: Diskette
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LIBRARY: GenBar
CLONE: 1683637
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STATE: CA
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLMAAQRYGRELRRMSDE 120
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GENERAL INFORMATION:
APPLICANT: APOPTOSIS TECHNOLOGY, INC.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: TAND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REPERBNCE: F137122
CURRENT APPLICATION NUMBER: PCT/US00/11864
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEO ID NOS: 20
SOFTWARE: PATENTIN VET. 2.1
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Indels
                                                                                                                                                                                               APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Mine Edwards, Jean Baptiste
APPLICANT: Dumas Mine Edwards, Jean Baptiste
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.051.PRO
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
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Pred. No. 1.1e-50;
1; Mismatches 0;
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Best Local Similarity 99.2%;
Matches 124; Conservative
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PCT-US00-11864-3
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Matches 126; Conserv
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Sequence 1. Application PC/TUS9715871
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
TITLE OF INVENTION: REGULATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
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                                                                                  158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
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GENERAL INFORMATION:
GENERAL RORSMEYER, STANLEY J
TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              965018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REPERENCE/DOCKET NUMBER: 9650
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US97-15871-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63146
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PCT-US97-15871A-1
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Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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56 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                   REGULATING APOPTOSIS,
SCREENING FOR COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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GRNERAL INFORMATION:
APPLICAMT: APOPTOSIS TECHNOLOGY, INC.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REPERENCE: F137122
CURRENT APPLICATION NUMBER: PCT/US00/11864
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 646; DB 1; Length 204; 75.0%; Pred. No. 2.5e-48;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR REG;
TILLE OF INVENTION: COMPOUNDS OF MAKING AND SCR;
TILLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: A7483
CURRENT APPLICATION NUMBER: US/09/580,523
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 646; DB 19; 75.0%; Pred. No. 1.9e-48; ive 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%
Matches 126; Conservative
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Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus US-09-580-523-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
PCT-US00-11864-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                 US-09-580-523-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM PC Compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15871A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R
REFERENCE/DOCKET NUMBER: 6029-1938
FREINTATION NUMBER: 6029-1938
TELEPOME (314) 727-5188
TELEPOME (314) 727-5188
TELEPOME (314) 727-5188
TELEPOME (A14) 727-5188
TELEPOME (A14) 727-5188
TELEPOME (A14) 727-5188
TELEPOME (A14) 727-5188
TELENGTH: 204 amino acid
STRANDEDNESS:
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US97-15871A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.4%; Score 646; DB 1; Best Local Similarity 75.0%; Pred. No. 2.5e-48; Matches 126; Conservative 13; Mismatches 23;
                                            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STRATE: MISSOURI
COUNTY: USA
ZIP: 63105
       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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Search completed: October 9, 2001, 16:02:05 Job time: 270 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

 protein search, using sw model OM protein

9, 2001, 15:54:04; Search time 28.81 Seconds October Run on:

(without alignments) 68.745 Million cell updates/sec

26 US-09-580-523-1\_COPY\_143\_168 145 1 QSSWTRVFQSWWDRNLGRGSSAPSQ Perfect score: Sequence:

BLOSUM62 Gapop 10.0 ,~Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query	Length	DB	ID	Description
п	120	82.8		7	A55671	bad protein - mous
7	57	39.3		7	A44062	genome polyprotein
m	54	37.2	-	~	C70752	probable ctpI prot
4	53	36.6		7	568691	neutrophil granule
S	53	36.6		N	E83006	two-component resp
9	23	36.6		~	T39479	histone transcript
7	53	36.6	3163	П	JQ1895	genome polyprotein
80	51	35.2		7	F45557	external glycoprot
6	50.5	34.8		7	F75357	hypothetical prote
10	20	34.5	144	7	S29946	surface qlycoprote
11	20	34.5	157	7	PQ0619	envelope protein -
12	20	34.5	243	7	B33329	cysteine-rich secr
13	20	34.5	264	7	T31521	hypothetical prote
14	. 50	34.5	299	7	B83081	
15	20	34.5	634	7	A48335	•
16	20	34.5	1170		TSHUP1	thrombospondin 1 p
17	20	34.5	1170	ď	A40558	thrombospondin 1 p
18	20	34.5		-	JN0545	genome polyprotein
19	20	34.5	m	~	JS0166	genome polyprotein
20	e.	34.1	335	~	T10074	cytochrome-c perox
21	49.5		358	<del>, -</del>	JQ1870	AL1 protein - toma
22	49			7	S29952	surface qlycoprote
23	49			7	PQ0626	envelope protein -
24	49	33.8		7	A24609	acidic epididymal
25	49			7	F84764	hypothetical prote
56	49	33.8		7	H83635	conserved hypothet
27 .	49	33.8		7	G83310	
28	49	33.8	741	7	D83633	
59	49	33.8	1148	7	T09073	splicing factor Si

lactase (EC 3.2.1.	surface glycoprote	hypothetical prote	envelope protein -	testicular protein	probable retroelem	genome polyprotein	DNA topology modul	hypothetical prote	mitochondrial proc	conserved hypothet	lactase (EC 3.2.1.	beta-qlycosidase c	hypothetical prote	hypothetical prote	· ~
S43719	S29947	F85949	PQ0620	JE0204	C84512	GNBVEV	A75513	T50944	800552	F82987	543721	S01169	D72701	T48709	T49363
7	~	7	7	7	~	-	7	7	Н	7	~	7	7	7	7
1918	225	236	241	243	1501	3054	170	426	462	691	1920	1926	110	202	119
33.8	33.1	33.1	33.1	33.1	33.1	33.1	32.4	32.4	32.4	32.4	32.4	32.4	32.1	32.1	31.7
49	48	48	48	48	48	48	47	47	47	47	47	47	46.5	46.5	4 6
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

A55671 bad protein

C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
B;Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A;Refatus: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-204 < YAN>
A;Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C;Keywords: heterodimer

Gaps ; 0 Length 204; 4; Indels 82.8%; Score 120; DB 2; 73.1%; Pred. No. 9.9e-10; 3; Mismatches Query Match 82.8% Best Local Similarity 73.1% Matches 19; Conservative

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1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26 δλ

С

Agrocation polyprotein - pepper mottle virus (strain California)

N;Contains: 29K protein; 34K protein; coat protein; cylindrical inclusion protein; he C;Species: pepper mottle virus
C;Species: pepper mottle virus
C;Species: pepper mottle virus
C;Accession: A44062
R;Vance, V.B.; Moore, D.; Turpen, T.H.; Bracker, A.; Hollowell, V.C.
N;Title: The complete nucleotide sequence of pepper mottle virus genomic RNA: compari A;Reference number: A44062; MUD:93033110
A;Title: The complete nucleotide sequence of pepper mottle virus genomic RNA: comparison: A44062; MUD:93033110
A;Residues: 1-3068 <VAN>
A;Residues: 1-3068 <VAN>
A;Residues: 1-3068 <VAN>
A;Residues: 1-3068 <VAN>
A;Cross-references: GB:M96425; NID:9332869; PIDN:AA46903.1; PID:9332870
C;Superfamily: tobacco etch virus genome polyprotein
C;Keywords: ATP; coat protein; cylindrical inclusion protein; genome-linked protein;
C;Keywords: ATP; coat protein #status predicted <KPP>
F;1289-743/Product: 29K protein #status predicted <KPP>
F;1287-1790/Product: cylindrical inclusion protein #status predicted <CIP>
F;1350-1331/Region: nucleotide-binding motif B
F;1330-1333/Region: DEXH motif
F;1791-2276/Product: nuclear inclusion protein a #status predicted <NIA>

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two-component response regulator NtrC PA5125 [imported] - Pseudomonas aeruginosa (str C; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Stecs: 15.5ep-2000 #sequence_revision 15.5ep-2000 #text_change 31-Dec-2000 (c; Accession: E83006 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  histone transcription regulator beta-transducin homolog - fission yeast (Schizosaccha C; Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
C;Accession: T39479
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ntrC; PA5125
C;Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB:AE004091; NID:q9951415; PIDN:AAG08510.1; GSPDB:GN
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A;Residues: 1-807 <LYN>
A;Cross-references: EMBL:AL031349; PIDN:CAA20478.1; GSPDB:GN00067; SPDB:SPBC15D4.03
A;Experimental source: strain 972h-; cosmid c15D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819 C;Genetics: A;Gene: SGP26 C;Senetics: C;Superfamily: cysteine-rich secretory protein 1 F;1-19/Pomain: signal sequence #status predicted <SIG> F;20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Gene: SPDB:SPBC15D4.03
A;Map position: 2
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476;
                                                                                                                                                                                                                                     Length 245,
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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11;
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Pred. No. 6.4;
6; Mismatches
                                                                                                                                                                                                                                                               Pred. No. 3.3;
5; Mismatches
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66.7%; Pred. No. 1
                                                                                                                                                                                                                                     Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     107 SSWSQAIQSWFDEYNDFDFGVGPKTPN 133
                                                                                                                                                                                                                                                                                                                                                  3 SSWTRVFQSWWDR----NLGRGSSAPS 25
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                                                                                                                                                                                                                                     Query Match 36.6%;
Best Local Similarity 37.0%;
Matches 10; Conservative
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Best Local Similarity 38.1%;
Matches 8; Conservative
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les 8; Conservative
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Matches
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R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E; Connor, R.; Davies, R.; Devinn, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.; Holroyd, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Bulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Accession: C70752
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-1632 <COL>
A; Residues: 1-1632 <COL>
A; Experimental source: strain H37Rv
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neutrophil granules matrix glycoprotein SGP28 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 1957 #sequencervision 13-Mar-1997 #text_change 17-Nov-2000
C;Accession: S68691; S74313; S68683
R;Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.
R;Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.
A;Title: SGP38, a novel matrix glycoprotein in specific granules of human neutrophils with Reference number: S68691; MUID:96186934
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A; Residues: 33-83;96-143;165-217;221-226 <KJL>
A; Residues: 33-83;96-143;165-217;221-226 <KJL>
A; Rasidues: 33-83;96-143;165-217;221-226 <KJL>
B; Kraetzschnar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuni Eur. J. Biochem. 236, 827-836, 1996
A; Ritle: The human cysteine-rich secretory protein (CRISP) family. Primary structure and A; Reference number: $68681; MUID:96270732
A; Accession: $68683
A; Status: pression: $68683
A; Status: pression: $68683
A; Status: pression: $7.107-245 <KRA>
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A;Residues: 1-245 <KALE>
A;Cross-references: EMBL:X94323; NID:g1213612; PIDN:CAA63984.1; PID:g1213613
A;Accession: S74313
                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable ctpI protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
        nuclear inclusion protein b #status predicted <NIB>
F;2277-2799/Product: nuclear inclusion protein b #status predicted <NIF
F;2800-3068/Product: coat protein #status predicted <CPT>
F;1906/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
                                                                                                                                                                                                        ;
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C;Superfamily: ATPase nucleotide-binding domain homology
F;1237-1406/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1632;
                                                                                                                                                   1; Length 3068
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                                                                                                                                    DB 7
                                                                                                                                             Score 57; DB 1
Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 2
Pred. No. 16;
1; Mismatches
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71.4%;
                                                                                                                                             Query Match 39.3%;
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                 1191 FESWWDEQVARGFTIP 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.2
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                               9 FQSWWDRNLGRGSSAP 24
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hypothetical protein - Deinococcus radiodurans (strain R1)
C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Species: Deinococcus radiodurans
C; Date: 0.3-Dec-1999 #sequence_revision 0.3-Dec-1999 #text_change 31-Mar-2000
C; Accession: F75557
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID:20036896
A; Accession: F75357
A; Status: preliminary
A; Residues: 1-328 < WHI>
A; Residues: 1-328 < WHI>
A; Residues: 1-328 < WHI>
A; Experimental source: strain R1
C; Genetics:
A; Genetics:
A; Map position: 1
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C;Species: feline immunodeficiency virus
C;Species: feline immunodeficiency virus
C;Species: feline immunodeficiency virus
C;Species: feline immunodeficiency virus
C;Species: S2946
R;Righy, M.A.
submitted to the EMBL Data Library, November 1992
A;Reference number: S2946
A;Reference number: S2946
A;Reference number: S2946
A;Reference number: DNA
A;Residues: 1-144 <RIC>
                                                                                                                                                                                                                                                                                                              Gaps
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C;Superfamily: feline immunodeficiency virus env polyprotein
C;Keywords: glycoprotein
                                                                                            NCBIP:89854)
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A;Molecule type: DNA
A;Residues: 1-855 <MAK>
A;Experimental source: strain TW2
A;Note: sequence extracted from NCBI backbone (NCBIN:89826, N
C;Superfamily: feline immunodeficiency virus env polyprotein
C;Keywords: glycoprotein; transmembrane protein
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Pred. No. 5;
0; Mismatches
                                                                                                                                                                                                                                               Score 51; DB 2
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                     DB '
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Pred. No. 9.9;
3; Mismatches
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56.2%;
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ilarity 56.2%;
Conservative
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Best Local Similarity 41.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        383 OSGSWIRTISSWKORN 398
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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A Residues: 2876-2892;292-2941;3118-3141 < TR2>

A Residues: 2876-2892;292-2941;3118-3141 < TR2>

A Residues: 2876-2892;292-2941;3118-3141 < TR2>

C Superfamily: tobacco etch virus genome polyprotein

C Keywords: ATP; coat protein; genome-linked protein; inclusion protein; nucleotide bind

C F;1-362/Product: Pl protein #status predicted < PIP>

F;363-820/Product: Plane component protein #status predicted < PIP>

F;3176-1175/Product: P3 protein #status predicted < PIP>

F;1176-1127/Product: Gytoplasmic inclusion protein #status predicted < PIP>

F;1328-1870/Product: Cytoplasmic inclusion protein #status predicted < CIP>

F;1398-1407/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                        genome polyprotein – turnip mosaic virus
N:Contains: coat protein; cytoplasmic inclusion protein; helper component protein; nucle
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A; Title: Molecular characterization and heterogeneity of feline immunodeficiency virus A; Reference number: A45557; MUID:92198230
A; Sctatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-3163 <NIC>
A; Residues: 1-3163 <NIC>
A; Cross-references: DDBJ:D10927; NID:g222660; PIDN:BAA01725.1; PID:g222661
A; Experimental source: strain Quebec
B; Tremblay, M.F.; Nicolas, O.; Sinha, R.C.; Lazure, C.; Laliberte, J.F.
J. Gen. Virol. 71, 2769-2772, 1990
A; Title: Sequence of the 3'-terminal region of turnip mosaic virus RNA and the capsid |
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A;Rosidues: 1554-2861,'G',2863-3163 <TRE>
A;Cross-references: GB:D10601; GB:D01090; NID:g222658; PIDN:BAA01452.1; PID:g222659
A;Accession: PQ0217
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                                                                                                                                                                                                                                                                                                                              C;Species: turnip mosaic virus, TuMV
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C;Accession: J01895; J01068; PQ0217
R;Nicolas, O.; Laliberte, J.F.
J. Gen. Virol. 73, 2785-2793, 1992
A;Tille: The complete nucleotide sequence of turnip mosaic potyvirus RNA.
A;Reference number: J01895; MUID:93057350
A;Accession: J01895
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C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C;Accession: F45557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F1871-1923/Product: p6K2 protein #status predicted <PKP>
F1924-2115/Product: VPg protein #status predicted <VPG>
F1924-2315/Product: wordear inclusion a protein #status predicted <NIA>
F2316-2358/Product: nuclear inclusion b protein #status predicted <NIA>
F2355-2875/Product: nuclear inclusion b protein #status predicted <NIB>
F;2876-3163/Product: coat (capsid) protein #status experimental <CAP>
F;1986/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: JQ1168; MUID:91073142
A;Accession: JQ1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1402-1405/Region: DEXH motif
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                                                               [||| || : ||
624 SSSWLRVSEGWW 635
                               SSSWTRVFQSWW 13
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F45557
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A; Cross-references: GB: AE004865; GB: AE004091; NID: 99950752; PIDN: AAG07900.1; GSPDB: GN
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A;Accession: B83081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ### B83081

Hypothetical protein PA4512 [imported] - Pseudomonas aeruginosa (strain PA01)

C. Species: Pseudomonas aeruginosa

C. Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C. Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C. Accession: B83081

C. Stover, C. K.; Pham, X. Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbic, J. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

Nature 406, 959-964, 2000
                                                                                                                                                                      hypothetical protein Y116ABC.23 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: D-oct-1999 #sequence_revision 29-oct-1999 #text_change 04-Mar-2000
C;Accession: T31521
R;McMurray, A.
submitted to the EMBL Data Library, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic inclusion protein - potato virus Y (strain O)
C;Species: potato virus Y, PVY
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 02-Feb-2001
C;Accession: A48335
R;Ohshima, K.; Inoue, A.K.; Shikata, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 42/3; 102/3; 178/3; 213/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-264 <WIL>
A; Cross-references: EMBL:AL117204; PIDN:CAB55155.1; CESP:Y116A8C.23
A; Experimental source: clone Y116A8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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A;Molecule type: DNA
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9.3;
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Pred. No. 9.3;
2; Mismatches
   105 TSWSSAIQSWYDEILDFVYGVGPKSPN 131
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224 TQGWATAFNRWFSRNVMAAAAAPN 247
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C, Genetics:
A, Gene: PA4512
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56.2%;
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Matches 7; Conservative
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Best Local Similarity
Matches 9; Conserv
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J. Gen. Virol. 74, 425-436, 1993
J. Title: Evolution of structural proteins of feline immunodeficiency virus: Molecular ep. A;Reference number: JQ2003; MUID:93187604
A;Accession: PQ0619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Jun-2000
C; Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Jun-2000
C; Accession: B33329; S68682
R; Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genomics 5, 527-534, 1989
A; Title: Cloning and mapping of a. testis-specific gene with sequence similarity to a specific componer: A33329; MUID:90129048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNÅ

A; Residues: 1-243 < KAS.>

A; Residues: 1-243 < KAS.>

A; Cross-references: GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883

B; Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuni

Br. J. Blochen. 236, 827-836, 1996

A; Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and

A; Reference number: S68681; MUID:96270732
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-243/Product: cysteine-rich secretory protein 2 type I #status predicted <MAT>
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                                                                                                                                       envelope protein - feline immunodeficiency virus (isolate UK 5) (fragment) C:Species: feline immunodeficiency virus C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999 C:Accession: PQ0619
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C;Keywords: envelope protein; glycoprotein
F;92/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 5
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Pred. No.
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A;Map position: 6p21-6qter
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37.0%;
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56.2%;
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Best Local Similarity 56.2.
Pest Local 9, Conservative
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A, Residues: 1-157 <RIG>
A, Cross-references: GB:X69495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QSSSWTRVFQSWWDRN 16
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41 OPGSWLRVISSWKORN 56
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Best Local Similarity
Matches 10; Conserv
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M.J.; K.; L

P.; Hickey, A.; Larbig,

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A; Residues: Genetics

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A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of the potatd A;Reference number: A48335; MUID:93119268
A;Accession: A48335
A;Status: preliminary
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Molecule type: 1-634 COHS>
A;Residues: 1-634 COHS>
A;Cross-references: GB:S51663; NID:9262852; PIDN:AAB24777.1; PID:9262853
A;Cross-references: GB:S51663; NID:9262852; PIDN:AAB24777.1; PID:9262853
A;Note: sequence extracted from NCBI backbone (NCBIN:121707, NCBIP:121709)
C;Superfamily: tobacco eacth virus genome polyprotein
C;Keywords: nucleotide binding; P-loop
F;85-92/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
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35 FSDWWDRQIQMGHTLP 50
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Search completed: October 9, 2001, 15:54:05 Job time: 235 sec

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; Entered [jdelaval 9-Oct-01 15:43]
09-580523-1A
MPQIPEPEPSEDEDSSAERGLGPSPACDGPSGGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIR
SRHSSYPAGTEDDEGWGEPEPFRGRSRAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQ
MRQSSSWTRVFQSWWDRNLGRGSSAPSQ1

; Entered [jdelaval 9-Oct-01 15:46] 09-580523-1B MFQIPEFEPSEQEDSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSHHGGAGAVEIR SRHSSYPAGTEDDEGWGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEFVDSFKKGLPRPKSAGTATQ MRQSSSWTRVFQSWWDRNLGRGSSAPSQ1

gar 2

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Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

Run on:

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GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                         Sequence Seq
       Sequence
                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR/KFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 112; DB 1;
100.0%; Pred. No. 5.9e-11;
iive 0; Mismatches 0;
                              US-09-472-971-1
US-08-785-429-2
US-08-996-366-2
US-08-996-366-2
US-08-335-409-3
US-09-335-409-3
US-09-335-409-3
US-08-638-1
US-09-004-713-1
US-09-698-551-6
US-08-698-551-6
US-08-649-341A-6
US-08-649-341A-6
US-08-649-341A-6
US-08-68-33-901B-6
US-08-833-901B-6
US-08-833-901B-6
US-08-833-901B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2411 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPAX: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: PATENTIN Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08665617
Patent No. 5663316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 NLWAAQRYGRELRRMSDEFVD 121
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Best Local Similarity 100.
Matches 21; Conservative
                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
   \tilde{\mathbf{v}}.\tilde{\mathbf{v}}.\tilde{\mathbf{v}}.\tilde{\mathbf{v}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{o}}.\tilde{\mathbf{
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-665-617-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-665-617-2
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Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 57, Appl
Sequence 1, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 26, Appli
Sequence 69, Appli
                                                                                                                                                                                                                                                                                      (without alignments)
16.637 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                 ; Search time 25.99 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-665-617-2
US-08-915-123-2
US-08-915-315-1
US-08-313-565-10
US-08-611-479-10
US-08-713-505A-55
US-08-733-505A-55
US-08-733-505A-55
US-08-733-505A-57
US-08-733-505A-12
US-08-733-505A-13
US-08-733-505A-13
US-08-733-505A-13
US-08-733-505A-14
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US-09-299-843A-40
PCT-US93-11153-40
US-09-147-923-2
US-08-680-326-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197339 segs, 20590346 residues
                                                                                                                                                                                                                                                                                                                                                                                     US-09-580-523-1_COPY_103_123
112
1 NLWAAQRYGRELRRMSDEFVD 21
                                                                                                                                                                                                                                             9, 2001, 15:52:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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Result Š ö

Gaps

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Length 168;
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APPLICANT: Yue, Henry
APPLICANT: La1, Preett
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 100.0%; Score 112; DB 3; Best Local Similarity 100.0%; Pred. No. 6e-11; Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: Fast SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
                                                                                                                                                                                                                                                                          PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08985335; Patent No. 6080847; GENERAL INFORMATION:
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: B111111 ings, Lucy J.
REGISTRATION NUMBER: 37.749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 NEWAAQRYGRELRRMSDEFVD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFVD 21
                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNORAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LIBRARY: SYNOF
; CLONE: 358673
US-08-985-335-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-985-335-7
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                                                                                                              APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
CORRESPONDENCE: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%; Score 112; DB 2; Length 168; larity 100.0%; Pred. No. 6e-11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Noil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
OURBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                           Sequence 2, Application US/08717123
Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 NLWAAQRYGRELRRMSDEFVD 123
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                                                                                                                                                                                                                                                                     STREET: 4370 La Jolla VI
CITY: San Diego
STATE: California
COUNTRY: United States
ZIF: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 168 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-717-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STREET: 31/7
TTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                           GENERAL INFORMATION:
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                         -08-717-123-2
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Gaps

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STRANDEDNESS: single
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                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                   RESULT 6
US-08-661-479-10
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                                                                                                                                                                                                                                                            100.0%; Score 112; DB 3; Length 168; 100.0%; Pred. No. 6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08333565
Patent No. 562852
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 102; DB 1; Length 23; 100.0%; Pred. No. 3e-10; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                               Score 112,
Pred. No. 6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 326-2400
TELEPRAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                   1 NLWAAQRYGRELRRMSDEFVD 21
           TELEBRAY: 650.845.4166
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDEF 19
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650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 23 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                21; Conservative
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                                                                                                                                                                ; LIBRARY: GenBank
; CLONE: 1683637
US-08-985-335-7
                                                                                                                                                                                                                                                                       Best_Local_Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 19; Conserv
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94301
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US-08-333-565-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-333-565-10
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Sequence 55, Application US/08733505A
Sequence 55, Application US/08733505A
Sequence 55, Application US/08733505A
Senser No. 5856445
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Sequence 10, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                       ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 102; DB 2;
Pred. No. 3e-10;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15726A-000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NEWAAQRYGRELRRMSDEF 21
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.1
Best Local Similarity 100.
Matches 19; Conservative
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41 NLWAAQRYGRELRRMSDEF 59
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                                                                                                                  1 NLWAAQRYGRELRRMSDEF 19
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Best Local Similarity 100.
Matches 19; Conservative
                                                                           Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 7/33.
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                        Local Similarity
hes 19; Conserv
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US-08-733-505A-58
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                                          Query Match
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Matches
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Sequence 56, Application US/08733505A

Sequence 56, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:
APPLICANT: CORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL.XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HARERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 2; Le
Pred. No. 8.2e-10;
                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILIG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       91.1%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                        965458
                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96545
TELECOMMUNICATION INFORMATION:
TELEPHOR: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAONE: (314) 727-5188
TELERAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 NLWAAQRYGRELRRMSDEF 59
                                                                                                                                                                                                                                                                                             LENGTH: 59 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                               . MOLECULE TYPE: peptide US-08-733-505A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-733-505A-56
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Query March

Query
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: Bcl-x/Bcl-2
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: APWASSEN and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                   /note= "Deduced amino acid sequence
of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Deduced amino acid sequence of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TIFE: FIDEPY GISK
COMPUTER: FIDEPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/33,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 15726A-000700
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFRANCE/COCKET NUMBER: 15726A-000700
TELECOMMUTCATION INFORMATION:
TELEFRANCE (415) 326-2420
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEMOTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-08-661-479-2
; Sequence 2, Application US/08661479
; Patent No. 5834209
         LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                      ) NAME/KEY: Protein
; LOCATION: 1..204
; OTHER INFORMATION:
US-08-333-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION:
US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BC1.x/BC1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 102; DB 2; Length 59
100.0%; Pred. No. 8.2e-10;
tive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTED
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: SMAITH, William M
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET UNMBER: 15726A-000700
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 2:
                                                                                  ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
: 7733 FORSYTH BLVD., SUITE 1400
ST. LOUIS
MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                 965458
                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96545
TELECOMUNICATION INFORMATION:
TELEPHONE: (314) 727-6188
TELEFRAX: (314) 727-618
TELEFRAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 NLWAAQRYGRELRRMSDEF 59
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-58
                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                    COUNTRY:
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US-08-333-565-2
                                             STATE:
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Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION: STANLEY J.
TITLE OF INVENTION: BELLAL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 102; DB 2; Length 204;
Pred. No. 3e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 965458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.18; Sco.
100.08; Pre
0;
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ATORNEYAGEWT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERCE/POCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFA: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                 35,197
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
  MISSOURI
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US-08-733-505A-13
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                        COUNTRY:
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                                            Gaps
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TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STRESSE: HOWELL & HAFERKAMP, L.C.
STREST: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUWRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: SELX./BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERRAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
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Pred. No. 3e-09;
91.1%; Score 102; DB 2; Length 204; 100.0%; Pred. No. 3e-09;
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                                          Indels
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APPLICATION NUMBER: US/08/733,505A
        100.0%; Pred. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               Sequence 1, Application US/08733505A Patent No. 5856445 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.1%; Sco.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654;
TELECOMMUNICATION INFORMATION:
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                          140 NLWAAQRYGRELRRMSDEF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 NLWAAQRYGRELRRMSDEF 158
                                                                                    1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NLWAAQRYGRELRRMSDEF 19
                 Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.1
Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ST. LOUIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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Query Match
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Gaps

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; TYPE: amino acid
; STRANDENESS:
; POPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13

Ouery Match
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
Qy 1 NLWAAQRYGRELRRMSDEF 19
Db 140 NLWAAQRYGRELRRMSDEF 158
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Search completed: October 9, 2001, 15:52:36 Job time: 151 sec

; 0

0; Gaps

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337, App
51026, A
567, App
10646, A
                                                                                                                                                                          10646, A
11563, A
18587, A
48287, A
53631, A
14309, A
3620, A
1432, A
18666, A
                                                                                        746, App
                                                                                    Sequence 746, Af Sequence 337, Af Sequence 51026, Sequence 10646, Sequence 11563, Sequence 48287, Sequence 53631, Sequence 53631, Sequence 1309, Sequence 1309, Sequence 1309, Sequence 1309, Sequence 36270, Sequence 36270,
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                                                                      Sequence
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APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Under Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.052.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR RILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: PRIOR LIPROPARE: PRIOR FILING DATE: SEQ ID NOS: 52153
PCT-USO1-14827-15394
PCT-USO1-14827-15396
US-09-649-866A-2290
US-09-875-195-746
US-09-758-453-337
PCT-USO1-08631-51026
US-09-758-466-567
US-09-803-110-110546
US-09-803-110-110543
PCT-USO1-08631-38702
PCT-USO1-08631-38702
PCT-USO1-08631-3831
US-09-902-540-14309
US-60-312-544-10009
PCT-USO1-08631-3631
US-09-902-540-14309
US-60-312-544-10009
US-60-312-544-10009
US-09-993-332A-1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 112; DB 5;
Pred. No. 2.1e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-834-366-16338
; Sequence 16338, Application US/09834366
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-922-378-2; Sequence 2, Application US/09922378; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 NLWAAQRYGRELRRMSDEFVD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bejanin, Stephane APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
      4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: HOMO &
US-09-834-366-16338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 125
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LENGTH: 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16338, A Sequence 2, Appl1 Sequence 2752, Ap Sequence 3, Appl1 Sequence 9711, Ap Sequence 13700, A
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Sequence 43907, A
Sequence 52397, A
Sequence 257, App
                                                                                                                                           Search time 36.31 Seconds (without alignments) 27.430 Million cell updates/sec
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17, App
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37140, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-922-378-2

US-09-922-378-2

US-09-902-540-9711

PCT-USG11-08631-38983

US-09-902-540-13700

US-09-902-540-13700

US-09-902-540-13700

US-09-908-378-40

PCT-USG11-08631-52397

US-09-758-475-257

PCT-USG11-08631-52397

US-09-934-455-162

US-09-902-540-13770

US-09-902-540-13770

US-09-803-110-9772

US-09-803-110-11897

PCT-USG11-08631-35041

US-09-831-366-26246

PCT-USG1-08631-3441466

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US-09-902-540-10014
PCT-US01-08631-37140
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US-09-927-796-64
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                                                                                                                                                                                                                                                                                                                                                                                    311045 seqs, 47428042 residues
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                                                                                                                                                9, 2001, 16:08:31
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Maximum Match 100%
Listing first 45 summaries
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1 NLWAAQRYGRELRRMSDEFVD 21

    protein search, using sw model

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Maximum DB seq length: 2000000000
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Match
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RESULT 6
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                            100.0%; Score 112; DB 5; Length 168; 100.0%; Pred. No. 2.9e-10; cive 0; Mismatches 0; Indels
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APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.42803
CURRENT APPLICATION NUMBER: US/09/922,378
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PAl38CT
CURRENT APPLICATION NUMBER: PCT/USO1/18569
CURRENT FILING DATE: 2001-06-07
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                               Sequence 2762, Application PC/TUS0118569 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09922378 GENERAL INFORMATION:
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                                                                                                                                                                         103 NLWAAQRYGRELRRMSDEFVD 123
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                                                                              Best Local Similarity 100.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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PCT-US01-18569-2762
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LOCATION: (146)
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LOCATION: (37)
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LENGTH: 201
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LENGTH: 204
US-09-922-378-2
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                                                               Query Match
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LOCATION: (41)...(93)

OTHER INFORMATION: Heat shock hsp70 proteins family proteins domain identified OTHER INFORMATION: Heat shock hsp70 proteins family proteins domain identified OTHER INFORMATION: of 9.51

NAME/KEY: DOMAIN OF 9.51

LOCATION: (1)...(450)

OTHER INFORMATION: Hsp70 protein domain identified by PFam, accession name OTHER INFORMATION: Hsp70, E-value=3.2e-153, PFam score of 522.4
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                                                                                                                                                                                                                                                                                                APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof CURRENT APPLICATION UNMERS: US/09/902,540
CURRENT APPLICATION OWNERS: 2001-07-10
                                                  Gaps
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Sequence 38993. Application PC/TUS0108631
Sequence 38993. Application PC/TUS0108631
SERVERAL INFORMATION:
TILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-049
CURRENT APPLICATION NUMBER: 09/40,217
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 38983
LENGTH: 483
    Length 204;
                                                Indels
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OTHER INFORMATION: Xaa = X or * as defined in Table 2
  Score 99; DB 5;
Pred. No. 4e-08;
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                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50;
                                                                                                                                                                                                                                                       ; Sequence 9711, Application US/09902540; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 16825 SEQ ID NO 9711
                                                                                                                        140 NLWAAQRYGRELRRMTDEF 158
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                                                                                           1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Myxococcus xanthus US-09-902-540-9711
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157 SLWIGHRWGKGLRRMHGE 174
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Best Local Similarity 50.0°
                                                  Conservative
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LOCATION: (1)...(483)
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ORGANISM: Homo sapiens
Query Match
Best Local Similarity
Matches 18; Conserv
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
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Pred. No. 23;
2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
FRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
FRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSLOM
SEQ ID NO 43907
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                     NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.5;
Pred. No. 17
                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 40: US-09-088-3378-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/USO1/08631 CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: 09/540,217 PRIOR FILING DATE: 2000-03-31 PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23 NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43907, Application PC/TUS0108631 GENERAL INFORMATION:
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    FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                           LENGTH: 380 amino acids
                       ATTORNEY/AGENT INFORMATION:
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38.1%;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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Best Local Similarity 38.1v
8, Conservative
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PCT-US01-08631-43907
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PCT-US01-08631-43907
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PCT-US01-08631-52397
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APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TTLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE OF INVENTION: WYSOCOCCUS Xanthus Genome Sequences and Uses Thereof CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13700
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Gray, Patrick W.
Schwelkart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                          Score 46; DB 1; Length 483;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 5;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/153,848 FILING DATE: 17-NOV-1993 APPLICATION NUMBER: US 07/977,452
                                                                                                                                                                                                                                                                              Sequence 13700, Application US/09902540 GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/09088337B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                          41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.18;
72.78;
                                                                                                                                                                 355 NIWSAEKYKAEDKRQRDK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Myxococcus xanthus US-09-902-540-13700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                        1 NLWAAQRYGRELRRMSDE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                       CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.1
Best Local Similarity 72.7
Matches 8; Conservative
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342 WAAVRHGRELK 352
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PCT-US01-08631-38983
                                                                                                                                                                                                                                                           US-09-902-540-13700
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US-09-088-337B-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 270;
                                   APPLICANT: Raccliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Reuber, Lynne
APPLICANT: Yelchmann, Jose Luis
APPLICANT: Yelchmann, Jose Luis
APPLICANT: Tu Guo-Liang
APPLICANT: Tu Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0024
CURRENT APPLICATION NUMBER: PCT/USO1/26189
CURRENT FILING DATE: 2001-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEO ID NOS: 464
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Riechmann, Jose Luis
APPLICANT: Riechmann, Jose Luis
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB
Pred. No. 33;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR PILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162, Application US/09934455 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana
PCT-US01-26189-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana
US-09-934-455-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dubell, Arnold
Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.4%;
40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.4%;
40.0%;
                      Adam, Luc
Ratcliffe, Oliver
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APPLICANT: Creelman, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 40.03
Matches 8; Conservative
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Keddie, James
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Best Local Similarity
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LENGTH: 270
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LENGTH: 270
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                                                                                                        MAME/KEY: DOMAIN
LOCATION: (13)...(33)
OTHER INFORMATION: ALPHA-2A ADRENERGIC RECEPTOR SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00558C, p-value=7.330e-09, raw score
OTHER INFORMATION: 6.54
                                                                                                                                                                                                                                                                                          PFam, accession name PCI, E-value=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-758-475-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Sequence 257, Application US/09758475
SEPERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM035
CURRENT APPLICATION NUMBER: US/09/758,475
CURRENT FILING DATE: 2001-01-11
FRIOR PEPLICATION NUMBER: 60/179,065
FRIOR PELLING DATE: 2000-01-31
FRIOR PELLING DATE: 2000-01-31
FRIOR PELLING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 466
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.8%; Score 43.5; DB 1; Length 681; 55.6%; Pred. No. 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                  NAME/KEY: DOMAIN

LOCATION: (421)...(509)

OTHER INFORMATION: PCI domain identified by PFam, acce
OTHER INFORMATION: 2.1e-13, PFam score of 58.0

NAME/KEY: misc_feature
LOCATION: (1)...(681)

OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-52397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NLWAAQRYGRELRRMSDEFV 20
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APPLICANT: Creelman, Robert
PEPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WAAQRYGRELRRMSD-EF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 55.6
Matches 10; Conservative
                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE LOCATION: (7)
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LENGTH: 100
                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                           FEATURE
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Job time: 381 sec
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US-09-803-110-9772

US-09-803-110-9772

Sequence 9772, Application US/09803110

SEQUENCE 9772, Application US/09803110

SEQUENCE 9772, Application US/09803110

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15490)D

CURRENT APPLICATION NUMBER: US/09/803,110

CURRENT APPLICATION NUMBER: US 09/739,449

PRIOR FILING DATE: 2000-12-19

PRIOR PELING DATE: 2000-02-23

PRIOR FILING DATE: 2000-02-23

PRIOR FILING DATE: 1999-12-01

WUMBER OF EXQ ID NOS: 13351

SEQ ID NO 9772

LENGHH: 262

LENGHH: 262
                                                                                                                                                US-09-902-540-13770

Sequence 13770, Application US/09902540

GENERAL INROMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hisen C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13770

LENGTH: 572
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  8; Indels
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Pred. No. 90;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB Pred. No. 46; 2; Mismatches
  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 9, 2001, 16:08:31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.9%;
Best Local Similarity 50.0%;
Matches 10; Conservative 1
                                                         1 NLWAAQRY-----GRELR 13
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Myxococcus xanthus
US-09-902-540-13770
                                      1 NLWAAQRYGRELRRMSDEFV
8; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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38 NIWAAYREGHEI 49
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Perfect score:

Sequence:

OM protein

on:

Scoring table:

Searched:

Database

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Mouse BAD BH3 doma Bc12 polypeptide B Bc12 polypeptide B Bc12 polypeptide B Bc12 polypeptide B BLM BH3 consensus Bc12 polypeptide B Human Bim-L mutant Human Bim-L mutant Human Bim-L mutant Human Bim-L mutant Human Bc1-2 intera Human Bc1-2 in
                                 Mutant BCL-XL/BCL-Shorter Mutant BCL-XL/BCL-Shorter mutane BAD bcl-x(L)/bcl-2 ass Murine BCL-XL/BCL-Mutant BCL-XL/BCL-Mutant BCL-XL/BCL-Mutant BCL-XL/BCL-Mutant BCL-XL/BCL-Mutant BCL-XL/BCL-Mutant BAD protein
                                                                                                                                                                                             Longer murine BAD
Mammalian Bad BC1-
BAD BH3 consensus
bC1-x(L)/bC1-2 ass
Human BAD BH3 doma
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BAD BH3 domain reg
BAD BH3 domain reg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBC6 protein for regulating cell death.
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AAB37028
AAB37046
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AAW98166
AAW98167
AAW98168
AAW98157
AAW98158
                                                   AAW61322
AAB70370
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AAB70369
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AAB70371
AAR95163
AAY05421
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AAB70380
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AAW98164
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                                                                                        AAR95168
                                                                                                          AAW61315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW32476 standard; Protein; 166 AA
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 96US-0665617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLON-) CLONTECH LAB INC.
 WPI; 1997-447980/41.
                                                                                                                                                                                               991.3
881.2
881.2
774.1
774.1
774.1
776.0
665.0
665.2
741.1
11.1
141.1
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141.1
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Xudong Y;
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 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Bad protein.
bcl-x(L)/bcl-2 ass
Bcl2 polypeptide B
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Human Bcl-xL/Bcl-2
Human cell prolife
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                                                                                                                     // Search time 44.37 Seconds
(without alignments)
28.693 Million cell updates/sec
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   412676 seqs, 60623988 residues
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Maximum Match 100%
Listing first 45 summaries
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1 NLWAAQRYGRELRRMSDEFVD 21
                                                                                      - protein search, using sw model
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AAW55779
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AAB37001
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AAB70368
AAB48287
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Maximum DB seq length: 2000000000
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Score

Result No.

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168 AA;

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The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBG6 which regulates cell death through interaction with Bc1-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death promoting polypeptide. Bad, the binding of which to Bcl-XI results in the induction of programmed cell death, i.e. apoptosis. Bad can be used in screening assays for compounds to treat or prevent diseases characterised by apoptotic cell death, such as neurodegenerative disorders, e.g. Alzheimer's and Parkinson's creebellar degeneration, and myelodysplastic syndromes, e.g. aplastic anaemia and ischaemic injury including myocardial infarction, stroke and reperfusion injury. Assays can also be used to obtain apoptosis enhancing compounds to revenent classases characterised by the loss of apoptotic cell death, such as cancers, e.g. lymphoma and hormone dependent tumours, autolimmune diseases, e.g. systemic lupus erythematosus and immune-mediated powerulonephritis and viral infections, e.g. herpesvirus, poxvirus, or adenovirus infection. Bad can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                    Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is the human Bcl-xL/Bcl-2 associated
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                 Score 112; DB 18;
Pred. No. 1.5e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           programmed cell death; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                             AAW55779 standard; Protein; 168
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100.0%;
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Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IDUN-) IDUN PHARM INC.
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                                                                                                                                                             166 AA;
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The present sequence is the human APOP-1 protein. This protein, which shares structural and chemical homology with Bc1-2, is involved in cell proliferation. Its coding sequence was isolated by screening a synovial tissue cDNA library using a computer search for amino acid sequence alignments. The gene and protein can be used in the treatment of various cancers, disorders with associated inflammation such as Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atheosolerosis, Crohn's disease, ulcerative colitis, diabetes mellitus, cmphysema, glomerulonephritis, gout, Graves' disease, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myosthenia gravis, myocardial or pericardial inflammation, osteoporosis, rheumatoid arwith associated apoptosis including AIDS and other trauma, disorders with associated apoptosis including AIDS and other infectious and genetic immunodeficiencies, meurodegenerative diseases such as Alzheimer's disease and Parkinson's diseases including cachexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide and polypeptide sequences of proteins associated with cell proliferation for diagnosis, prevention and treatment of e.g. cancer, acquired immunodeficiency syndrome, and Parkinson's disease -
                                    Gaps
                                                                                                                                                                                                                                                                                                                      Human; cell proliferation; APOP-1; cancer; inflammation; infection; trauma; neurodegenerative disease; ischaemic injury; wasting disease.
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Length 168;
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100.0%; Pred. No. 1.6e-10;
iive 0; Mismatches 0;
100.0%; Score 112; DB 19;
100.0%; Pred. No. 1.6e-10;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lal P,
                                                                                                                                                                                                                                                                                       Human cell proliferation protein APOP-1.
                                                                                                                                                                                     AAB13512 standard; protein; 168 AA
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                                                                                     1 NLWAAQRYGRELRRMSDEFVD 21
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Query Match 100.

Best Local Similarity 100.
Matches 21; Conservative
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hes 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-451230/39
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated or synthetic polypeptide (I) Comprising a less than full length amino acid sequence of a mutant (I) Comprising a less than full length amino acid sequence of a mutant fragment, which contains amino acid substitutions at Seril8 of a human BAD. Seril5 of a murine BAD (longer murine BAD) or Seril3 of a murine BAD (shorter murine BAD) or Seril3 of a murine BAD (shorter murine BAD) or Seril3 of a murine BAD (shorter murine BAD) or Seril3 of a murine BAD (shorter murine BAD) or Seril3 of a murine BAD (shorter murine BAD) or Seril3 of a murine and interpretation antischaemic, vulnerary, cytostatic, antiviral, antischaemic, vulnerary, cytostatic, antiviral, antischaemic, vulnerary, cytostatic, antiviral, antischaemic, uninterpretation or inhibitor. BAD polypeptides and drugs for activity that promote cell survival or apoptosis. Other uses include inducting or inhibiting apoptosis in a cell. Candidate compounds inducting or inhibiting apoptosis in a cell. Candidate compounds inducinely diseases, ischaemic cell immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claimed human BAD mutant amino acid sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                         Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis; immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary; cytostatic; antiivtal; antiarthritic; antiinflammatory; wound healing; immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer; immunosuppressive; reperfection of elsease; viral infection; ischaemic cell death; reperfection cell death; reperfection cell death; arthritis; infertility; lymphoproliferative condition; inflammation; autolimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                               Human BAD mutant amino acid sequence SEQ ID NO:1.
                                                                                                                                                                      AAB70368 standard; protein; 168 AA.
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                       103 nlwaaqrygrelrrmsdefvd 123
1 NLWAAQRYGRELRRMSDEFVD 21
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                                                                                                                                                                                                                                                                          02-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                 AAB70368
                                                                                                                      RESULT
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The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKPL, SKP2), SKP2-like proteins (EF) and CUL-1 (a member of the cullin, CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                        S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax; Bad; Bc1-2; tumour; cytostatic.
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Pred. No. 1.6e-10;
Mismatches 0;
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                                                                                                                               AAB48287 standard; protein; 168 AA.
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103 nlwaaqrygrelrrmsdefvd 123
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N-PSDB; AAC84599.
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                   Human Bad protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200075184-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-1997
                                                                                                                                                                                                                       02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-2000.
                                                                                                                                                                           AAB48287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                        AAB48287
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Gaps

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Length 168; Indels

100.0%; Score 112; DB 22; 100.0%; Pred. No. 1.6e-10; ive 0; Mismatches 0;

21; Conservative

Query Match Best Local Similarity Matches 21; Conserv

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New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                        Huang Z, Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 17; 74pp; English.
    stroke; myocardial infarction.
                                                                                                                                                                                                                                                              (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                            06-APR-2000; 2000WO-US09352.
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-679325/66.
                                                                                       WO200059526-A1
                                                  Homo sapiens.
                                                                                                                                                                                                                   07-APR-1999;
                                                                                                                                  12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR95155-67 represent epitopes derived from the murine bcl.x(L)/Dcl-2 associated death promoter (Bad) polypeptide (see also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and bcl-x proteins and regulates cell death. It has homology to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad has been found to hybridise to bcl-x(L) and bcl-2 in yeast two hybrid assays and in vivo in mammalian cells. Overexpressed Bad counters the death inhibitory activity of bcl-x(L), but is much less effective at countering the death inhibitory activity of bcl-x(L), and its also counters the death repressor cell death induced by cytokine deprivation in an IL-3 dependent activity of bcl-x(L), and its also counters the death repressor activity of bcl-x(L), and its also counters the death repressor activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L). Bad may be used to identify agents which inhibit its binding to bcl-x(L) or bol-x(L) to form heterodimers. Such agents may be used to treat
                                         Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke; polypeptide; bcl-x; cell death; regulate; BHI; apoptotic cell death; cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS; neurodegenerative disease; senescence; ischaemia; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter useful to treat neoplasia and apoptosis and to identify agents inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; norsmall lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rm heterodimers. Such agents may be used to tre diseases, immunodeficiency diseases, e.g. AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 17;
Pred. No. 7.7e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bcl2 polypeptide BH3 domain peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 103; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.
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                                                                                                                                                                                                                                                                                                                     94US-0333565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB37001 standard; peptide;
                                                                                                                                                                                                                                                                              95WO-US14246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 nlwaaqrygrelrrmsdef 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               senescence or ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-251465/25.
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Les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                                                                                                                                                                                                                                                                              31-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                       Korsmeyer SJ;
                                                                                                                                                 Mus musculus
                                                                                                                                                                                             WO9613614-A1
                                                                                                                                                                                                                                                                                                                     31-OCT-1994;
                                                                                                                                                                                                                                    09-MAY-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2001
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached

to the N-terminus of the peptide, or a side chain of the peptide where

the functional group of the side chain is NH2 or OH; or X = O or NH,

when the R-X group is attached to the C-terminus of the peptide, or a

constant of the peptide, where the side chain functional group is COOH

constant of R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

con two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally

con two double bonds, cyclobutyl, cyclopentyl, cyclobexyl optionally

consolubstituted with a 1-5C straight or branched chain alkyl group,

consolubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-B37058 represent examples

consolubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides represent analogues

cof the peptide portion of the conjugate. The peptides represent analogues

cof a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

the BH3 domain of the cell death agonist Bdd. The peptide conjugate is

cerversing B cell lymphoma/leukenia 2 (Bcl-2)-mediated blockage of

the BH3 domain of the cancer cells it is also useful for inhibiting Bcl-2

conpugate is cancer cells. It is also useful for inhibiting a cute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

conjugate is also useful for treating disorders characterized by

conjugate is also useful for treating disorders characterized by

immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.1%; Score 102; DB 21;
100.0%; Pred. No. 8.8e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl2 polypeptide BH3 domain peptide #2.
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Matches 19; Conservative
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Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

Bcl2 polypeptide BH3 domain peptide #3.

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached to the herein and the peptide where the the relation of the peptide where the functional group of the spetide chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkxyl, cyclohexyl optionally nonesubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of the peptide portion of the conjugate. The peptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (BCI-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting BCI-2 cfunction. In particular, the peptide conjugate is useful for treating a cancer characterized by cancer cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      express Bol-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ф
cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increased apoptosis, e.g. neurodegenerative disorders, acquired
immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                         Lu Z;
                                                                                                                                                                                                                                                                                                                                                                                                         Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 17; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                           (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                       Wang J, Zhang Z,
                                                                                                                                                                                                                                                                     06-APR-2000; 2000WO-US09352.
                                                                                                                                                                                                                                                                                                                 99US-0128202
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679325/66.
                                                                                                                                                                             WO200059526-A1.
                                                                                                                                                                                                                                                                                                                 07-APR-1999;
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                         Huang Z,
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New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

cell

Claim 18; Page 17; 74pp; English.

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Huang Z, Wang J, Zhang Z, Shan S,

WPI; 2000-679325/66.

(UYJE-) UNIV JEFFERSON THOMAS

99US-0128202.

07-APR-1999;

06-APR-2000; 2000WO-US09352.

WO200059526-A1. Homo sapiens.

12-OCT-2000

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Matches
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                                     91.1%; Score 102; DB 21; Length 26; 100.0%; Pred. No. 8.8e-10; ive 0; Mismatches 0; Indels
                                                                                                                                                                              AAB37003 standard; peptide; 27 AA.
                                                                                      1 NLWAAQRYGRELRRMSDEF 19
                                                                                                      19; Conservative
                                                 Best Local Similarity
26 AA;
                                      Query Match
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28-FEB-2001 (first entry)

AAB37003;

SX X X E

RESULT AAB37003

Matches

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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=0, when the R-X group is attached
to the N-terminus of the peptide, or a side chain of the peptide where
the functional group of the side chain is NH2 or OH; or X = O or NH,

the functional group of the side chain is NH2 or OH; or X = O or NH,

c the functional group is attached to the C-terminus of the peptide, or a

cc side chain of the peptide, where the side chain functional group is COOH

cor CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one

cc two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

cc two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

cc two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally

cc two peptide portion of the conjugate. The peptides represent examples

cc the peptide portion of the conjugate. The peptides represent analogues

cc the peptide portion of the conjugate. The peptide conjugate is

cc the BH3 domain of the cell death agonist Bad. The peptide conjugate is

cc the BH3 domain of the cell death agonist Bad. The peptide conjugate is

cc reversing B cell lymphoma/leukenia 2 (Bcl-2)-mediated blockage of

capoptosis in cancer cells. It is also useful for inhibiting Bcl-2

cc function. In particular, the peptide conjugate is useful for treating a

consumption of the conjugate is useful for treating a

consumption of the conjugate is useful for treating a

consumption of a concer characterized by cancer cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          express BGL-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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100.0%; Pred. No. 9.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB37056 standard; peptide; 27 AA.
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AAB37056
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The invention relates to a peptide conjugate having the formula:

(R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a conditional group of the peptide, where the side chain functional group is COOH or CONH2, and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or CONH2, and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or CONH2, and R = 2-18C straight or branched chain alkyl group, or benzyl. The peptides ABB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a BCl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is reversing B cell lymphoma/leukemia 2 (BCl-2)-mediated blockage of a poptionis in cancer cells. It is also useful for inhibiting BCl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by
                                                                                                                                                                          cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leuemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
                                                                                                                                                      neuroprotective; anti-HIV; virucide; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lncreased apoptosis, e.g. neurodegenerative disorders, acquired
lmmunodeficlency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                          polypeptide BH3 domain peptide #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang J, Zhang Z, Shan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 19; 74pp; English.
                                                                                                                                                                                                                                                              stroke; myocardial infarction
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                                                               28-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                   WO200059526-A1.
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                      Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
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1 NLWAAQRYGRELRRMSDEF 19 

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AAB37055 standard; peptide; 28 AA.

AAB37055;

28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #55.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; 

stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1.

12-OCT-2000.

06-APR-2000; 2000WO-US09352.

99US-0128202. 07-APR-1999;

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ŝ Shan Zhang Z, Wang J, Huang Z,

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WPI; 2000-679325/66.

Щ New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

Claim 18; Page 19; 74pp; English.

The invention relates to a peptide conjugate having the formula:

(R.X)n-Peptide where n = 1-10; X = C-O, when the R.X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH2 or OH; or X = O or NH, when the R.X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl ben express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

28 AA; Sequence

Gaps .; 0 Length 28; Indels 91.1%; Score 102; DB 21; 100.0%; Pred. No. 9.5e-10; ive 0; Mismatches 0; Query Match Best Local Similarity 100.0 Matches 19; Conservative

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death regulator) proteins, having an amino acid other than Ser at present required to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral infection and autoimmune disease. Polymucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease. Polymucleotide sequences encoding proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is determined by measuring relative amounts of phosphorylated and non-phosphorylated bab, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not beterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family corrections in the cytosol, thus promoting cell survival. The mutants with
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                                                                                                                                                                                                                                                                        Mutant BCL-XL/BCL-2 associated cell death regulator #4.
                                                                                                                                           AAW61319 standard; Protein; 59 AA.
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1 NLWAAQRYGRELRRMSDEF 19
                     2 nlwaagrygrelrrmsdef 20
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The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at cosition 112 and/or 136, relative to the mutine BAD 204 as sequence. The position 112 and/or 136, relative to the mutine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, contrained by proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in 'drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is the phosphorylated and non-phosphorylated and non
                                                                                                                                                                                                                                                                                                                                                                                                        Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
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                                                                                                                                                                                                                                                                                                                                                   Mutant BCL-XL/BCL-2 associated cell death regulator #5.
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100.0%; Pred. No. 2.1e-09;
iive 0; Mismatches 0;
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1 NLWAAQRYGRELRRMSDEF 19
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dark regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 as sequence. The position 112 and/or 136, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein about 1417 (2) insion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, cancer, viral infection, lymphoproliferation, arthritis, infertility, and autolimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, continued by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunosassys. Mutant BAD proteins have phosphorylated and the specified Ser, forming a product that does not become phosphorylated on the specified Ser, forming a product that does not become phosphorylated on the specified Ser, forming a product that does not become phosphorylated by EU-2 or BCL-XL but instead binds to 14-3-3 family contains in the express), thus promoting cell survival. The mutants with
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                                                                                                                                                                                                                                                                                  Mutant BCL-XL/BCL-2 associated cell death regulator #6.
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death regulator) proteins, having an amino acid other than Ser at position 112 and/or 185, relative to the murine BAD 204 as sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD
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100.0%; Pred. No. 2.1e-09;
tive 0; Mismatches 0;
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Sequence 18, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 12, Appl Sequence 13, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 15, Appl Sequence 16, Appl Sequence 16, Appl

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Run on:

Sequence:

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Database

10 8 4 5 9 6 9 6 9 6 9

Result

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APPLICANT: Netesheim, David
APPLICANT: Meadows, Bob
APPLICANT: Meadows, Bob
APPLICANT: Clainicank, Ed
APPLICANT: Clainicank, Ed
APPLICANT: Clainicank, Ed
APPLICANT: Chang, Haichao
APPLICANT: Mary Haichao
APPLICANT: Mary Kerry
APPLICANT: Joseph, Mary K.
APPLICANT: 
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US-09-656-399-17

US-09-656-399-18

US-09-656-399-18

US-09-656-399A-10

US-09-656-399A-17

US-09-656-399A-19

US-09-656-399A-19

US-09-656-399A-19

US-09-716-395-20

US-09-716-395-20

US-09-716-395-29

US-09-375-257-2

US-09-375-37-32-1

US-09-386-339-15

US-09-656-399-15
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US-09-716-395-24
US-09-716-395-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30, Application US/09656399 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abbott Laboratories
Fesik, Steven
Petros, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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(cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-656-399A-30
US-09-16-395-36
US-09-656-399A-29
US-09-656-399A-28
US-09-656-399A-28
US-09-656-399A-27
US-09-656-399A-27
US-09-656-399A-27
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Maximum Match 100%
Listing first 45 summaries
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1 NEWAAQRYGRELRRMSDEFVD 21
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Maximum DB seq length: 200000000
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APPLICANT: Swift, Kerry M.
APPLICANT: Matayoshi, Edmund
APPLICANT: Atayoshi, Edmund
APPLICANT: Anang, Haichao
TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
TITLE OF INVENTION: THE RGE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6730.US.OI
CURRENT APPLICATION NUMBER: US/09/656,399A
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 31
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TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICT TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS FILE REFERENCE: 6370.US.Ol.
CURRENT APPLICATION NUMBER: US/09/656,399
CURRENT APPLICATION NUMBER: US/09/656,399
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pred. No. 2.3e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Wild-type human BAD peptide US-09-656-399-29
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Meadows, Robert P.
Joseph, Mary K.
Oleijiczak, Edward T.
Petros, Andrew M.
Nettesheim, David G.
                                                                                                                                                                                                                         Abbott Laboratories
Fesik, Steven
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                                      1 NLWAAQRYGRELRRMSDEFVD 21
                                                             1 NLWAAQRYGRELRRMSDEFVD 21
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Nettesheim, David
Meadows, Bob
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Zhang, Haichao
Ng, ShiChung
Swift, Kerry
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Best Local Similarity 100.
Matches 21; Conservative
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US-09-656-399A-29
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LENGTH: 22
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LENGTH: 22
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APPLICANT: Joseph, Mary K.
APPLICANT: Oleijiczak, Edward T.
APPLICANT: Oleijiczak, Edward T.
APPLICANT: Petros, Andrew M.
APPLICANT: Wetteshelm, David G.
APPLICANT: Matayoshi, Edmund G.
APPLICANT: Matayoshi, Edmund APPLICANT: Matayoshi, Edmund APPLICANT: Thang, Haichao TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6730.US.OI
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APPLICANT: Feets, Andrew W.
APPLICANT: Veets, Andrew W.
APPLICANT: Voon, Ho Sup
TITLE OF INVENTION: David G.
TITLE REPERENCE: 6752.US OI
CURRENT APPLICATION NUMBER: US/09/716,395
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FAA+FOOT
SED TO NOS: 37
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ilarity 100.0%; Pred. No. 2.2e-10;
Conservative 0; Mismatches 0;
                 Pred. No. 2.2e-10;
Mismatches 0;
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Pred. No. 2.2e-10;
Mismatches 0;
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; OTHER INFORMATION: synthetic peptide
US-09-656-399A-30
                                                                                                                                                                                                                         Sequence 30, Application US/09656399A GENERAL INFORMATION:
100.0%; Prr
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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                 Best Local Similarity 100.
Matches 21; Conservative
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SOFTWARE: FastSEQ for
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LENGTH: 21
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NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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Matayoshi, Edmund
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Matches 21; Conservative
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SEQ ID NO 28
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LENGTH: 24
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APPLICANT: Petros, Andrew M.
APPLICANT: Petros, Andrew M.
APPLICANT: Nettesheim, David G.
APPLICANT: Matayoshi, Edmund
APPLICANT: Zhang, Haichao
TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
TITLE OF INVENTION: THE ST. TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6730.US.01
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APPLICANT: Metucak, Ed
APPLICANT: Olejniczak, Ed
APPLICANT: Olejniczak, Ed
APPLICANT: Olejniczak, Ed
APPLICANT: Swift, Rerry
APPLICANT: Swift, Kerry
APPLICANT: Watayoshi, Ed
APPLICANT: Matayoshi, Ed
APPLICANTON: THE BCL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6370-US-Ol
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                 100.0%; Score 112; DB 20;
100.0%; Pred. No. 2.3e-10;
iive 0; Mismatches 0;
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Pred. No. 2.4e-10;
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; OTHER INFORMATION: synthetic peptide
US-09-656-399A-29
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; Sequence 28, Application US/09656399A
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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Meadows, Robert P.
Joseph, Mary K.
Oleijiczak, Edward T.
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100.0%; Pr
tive 0;
                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFVD 21
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Petros, Andrew
Nettesheim, David
Meadows, Bob
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                                                                                 Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity
Matches 21; Conservat
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APPLICANT:
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APPLICANT: Joseph, Mary K.

TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
CURRENT APPLICATION NUMBER: US/09/656,399
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 30
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ilarity 100.0%; Pred. No. 2.6e-10;
Conservative 0; Mismatches 0;
                                                                                                                               Score 112; DB 20;
Pred. No. 2.4e-10;
); Mismatches 0;
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FastSEQ for Windows Version 4.0
                    ; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-656-399A-28
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Joseph, Mary K.
Oleijiczak, Edward T.
Petros, Andrew M.
Nettesheim, David G.
                                                                                                                             100.0%; Sc
100.0%; Pr
tive 0;
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Fesik, Steven
Petros, Andrew
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                                                                                                                                                                                                                      1 NEWAAQRYGRELRRMSDEFVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nettesheim, David
APPLICANT: Meadows, Bob
APPLICANT: Olejniczak, Ed
APPLICANT: Zhang, Haichao
APPLICANT: Shang, Haichao
APPLICANT: Swift, Kerry
APPLICANT: Matayoshi, Ed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NLWAAQRYGRELRRMSDEFVD 21
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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APPLICANT: Netteshaim, David
APPLICANT: Netteshaim, David
APPLICANT: Netteshaim, Boavid
APPLICANT: Olejhiczak, Bd
APPLICANT: Olejhiczak, Ed
APPLICANT: Zhang, Haichao
APPLICANT: Zhang, Haichao
APPLICANT: Saift, Kerry
APPLICANT: Matayoshi, Ed
APPLICANT: Matayoshi, Ed
APPLICANT: JOSEPH, MATY K.
TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6370.US.01
CURRENT APPLICATION NUMBER: US/09/656,399
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
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                                         Petros, Andrew
Nettesheim, David
Meadows, Bob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
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Best Local Similarity
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; OTHER INFORMATION:
US-09-656-399-17
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COTHER INFORMATION:
US-09-656-399-18
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APPLICANT: Netesheim, David
APPLICANT: Netesheim, David
APPLICANT: Neadows, Bob
APPLICANT: Olejniczak, Ed
APPLICANT: Zhang, Haichao
APPLICANT: Swift, Kerry
APPLICANT: Swift, Kerry
APPLICANT: Matayoshi, Ed
APPLICANT: Ma
TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6730.US.01
CURRENT APPLICATION NUMBER: US/09/656,399A
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 31
SSC ID NO 27
LENGIH: 24
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100.0%; Pred. No. 2.7e-10;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6e-10;
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100.0%; Pred. No. 2.6
Live 0; Mismatches
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0S-09-656-349-17
; Sequence 17, Application US/09656399
; GENERAL INFORMATION:
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Fesik, Steven
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Nettesheim, David
Meadows, Bob
Olejniczak, Ed
Zhang, Haichao
Ng, ShiChung
Swift, Kerry
Matayoshi, Ed
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.6
Matches 21; Conservative
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Best Local Similarity 100.0
Matches 21; Conservative
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Gaps

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Indels

Length 25;

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APPLICANT: Olejniczak, Bob

APPLICANT: Olejniczak, Bob

APPLICANT: Zhang, Haichao

APPLICANT: Zhang, Haichao

APPLICANT: Swift, Kerry

APPLICANT: Worshi, Ed

APPLICANT: Matayoshi, Ed

APPLICANT: Joseph, Mary K.

ITILE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS

TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS

TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS

FILE REPRENCE: 6370, US-01

CURRENT APPLICATION NUMBER: US/09/656,399

CURRENT FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Faster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        These sequences were chemically synthesized based on the naturally occurring human BAD protein
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Pred. No. 2.7e-10;
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; 0

Gaps

;

Indels

21

Length 25;

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OTHER INFORMATION: These sequences were chemically synthesized based COTHER INFORMATION: on the naturally occurring human BAD protein US-09-656-399-20
                                                                                                                                                           100.0%; Score 112; DB 20;
100.0%; Pred. No. 2.7e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEFVD 21
                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                    1 NLWAAQRYGRELRRMSDEFVD
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Best Local Similarity 100.0
Matches 21; Conservative
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 21; Conserv
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APPLICANT: Zhang, Haichao
APPLICANT: Shichung
APPLICANT: Swift, Kerry
APPLICANT: Matayoshi, Ed
APPLICANT: Joseph, Mary K.
TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
TITLE OF INVENTION: THE BCL-2 FAMILY OF PROFEINS
FILE REFERENCE: 6370.US.01
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS FILE REFERENCE: 6370.US.01
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Pred. No. 2.7e-10;
); Mismatches 0;
 Mismatches
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                                                                                                                                                       Sequence 19, Application US/09656399 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09656399
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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100.0%; Pr/
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                                                   1 NLWAAQRYGRELRRMSDEFVD 21
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                                                                                                                                                                                               Abbott Laboratories
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Nettesheim, David
Meadows, Bob
                                                                                                                                                                                                                                                 Nettesheim, David
Meadows, Bob
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Zhang, Halchao
Ng, ShiChung
Swift, Kerry
Matayoshi, Ed
Joseph, Mary K.
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Best Local Similarity 100.
Matches 21; Conservative
21; Conservative
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Petros, Andrew
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NUMBER OF SEQ ID NOS:
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SEQ ID NO 20
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APPLICANT: Pesik, Stephen F.
APPLICANT: Meadows, Robert P.
APPLICANT: Meadows, Robert P.
APPLICANT: Joseph, Mary K.
APPLICANT: Joseph, Mary K.
APPLICANT: Deseph, Mary K.
APPLICANT: Detros, Andrew M.
APPLICANT: Metayosh, Edward T.
APPLICANT: Matayosh, Edward G.
APPLICANT: Matayosh, Edmund
APPLICANT: APPLICANTON: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF TITLE OF INVENTION: THE ELL-2 FAMILY OF PROTEINS
FILE REFERENCE: 6730.US.0.1
CURRENT APPLICATION NUMBER: US/09/656,399A
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 31
SOGTWARE: FastSEQ for Windows Ver-'
SEQ ID NO 10
LENGTH: 25
TYPE: --
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Pred. No. 2.7e-10;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: synthetic peptide US-09-656-399A-10
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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us-09-580-523-1\_copy\_103\_123.rsp

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October 9, 2001, 15:55:20 ; Search time 17.79 Seconds (without alignments) 40.436 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
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US-09-580-523-1\_COPY\_103\_123 112 1 NLWAAQRYGRELRRMSDEFVD 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 Total number of hits satisfying chosen parameters:

93435 seqs, 34255486 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

		ď			SUMMARIES		
Result No.	Score	Query Match	Query Match Length	DB	OI.	Description	tion
1	112	0	168	-	BAD_HUMAN	092934	homo sapien
7	102	91.1	204	٦	BAD_MOUSE	061337	mus musculu
m	47.5	42.4	595	П	VG13_BPMD2	064206	mycobacteri
4	46.5	41.5	503	٦	MTBR_BPRH1	P09915	bacteriopha
2	45	40.2	287	7	PRFA_POLPE	P21259	polyorchis
9	45	40.2	370	П	AROG_YEAST	P32449	saccharomyc
7	45	40.2	377	٦	APJ_MOUSE	- 80vw60	mus musculu
æ	45	40.2	380	Н	APJ_HUMAN	P35414	homo sapien
6	45	40.2	380	-	APJ_MACMU	097666	macaca mula
10	44	39.3	1008	٦	DPOL_HSVE2	P52367	equine herp
11	43	38.4	220	П	6PGL_THEMA	800x60	thermotoga
12	43	38.4	370	П	AROG_CANAL	P79023	candida alb
13	43	38.4	463	-	Y030_NPVAC	P41434	autographa
14	43	38.4	905	-	ZO3_MOUSE	Q9qxy1	mus musculu
15	43	38.4	1557	Н	LML1_CAEEL	018823	caenorhabdi
16	42		185	٦	RRF_THEMA	Q9x1b9	thermotoga
17	42		432	П	TIG_ECOLI	P22257	escherichia
18	42		501	П	TDT_ONCMY	092089	oncorhynchu
19	42		653	-	HT2A_HUMAN		homo sapien
20	42		715	П	DCLY_SALTY		salmonella
21	42		752	-	NEC1_RAT	P28840	rattus norv
22	41		391	٦	UBIF_ECOLI	P75728	escherichia
23	41	36.6	629	-	DNAK_HALCU	P42372	halobacteri
24	41		704	٦	KPC1_CAEEL	P34722	caenorhabdi
25	41		861	-	GCR3_YEAST	P34160	saccharomyc
56	41		883	7	CAPP_ECOLI	P00864	escherichia
27	41		4466	٦	DYHC_ANTCR	. P39057	anthocidari
28	40.5		143		YXAD_BACSU	P42103	bacillus su
29	0		629	Н	YYBT_BACSU	P37484	bacillus su
30	40		188	Н	ADML_BOVIN	_	bos taurus
31	40	35.7	202	П	TENI_BACSU	P25053	bacillus su
32	40	35.7	261	7	YGFG_ECOLI	P52045	escherichia
33	40	35.7	380	Т	PHLC_TRYCR	015886	trypanosoma

RESULT 2 BAD\_MOUSE

P55308 hordeum vul P11071 escherichia P51067 salmonella P52323 borrelia bu P32868 reovirus (t P35318 homo sapien P55304 clostridium Q85230 pseudorabie Q91ti4 neisseria m Q91y13 neisseria m P36601 schizosacch P03525 reovirus (t		HUMAN STANDARD; PRT; 168 AA.  OV-1997 (Rel. 35, Created)  OV-1997 (Rel. 35, Created)  OV-1997 (Rel. 35, Created)  OV-1997 (Rel. 36, Last sequence update)  PROTEIN (BCL-2 BINDING COMPONENT 6).  SABJEGOR BELL248.  SABJEGOR BELL248.  SABJEGOR BELL248.  SABJEGOR BELL248.  SABJEGOR BELL248.  SABJEGOR BELL248.  SABJEGOR BELL249.  THERES AFFECTING THE ENERGINE SABJEGOR HOMO.  TAX L1 Z. THANG BELL27.  THERES AFFECTING THE LEVEL  STANDARG CELL DEATH. SOCCESSTHING THE LEVEL  STANDARG TO BCL. X(L) AND BCL. 2, THERESTA AFFECTING THE LEVEL  STANDARG TO BCL. X(L) AND BCL. 2, THERESTA AFFECTING THE LEVEL  STANDARG TO BCL. X(L) AND BCL. 2, THERESTA AFFECTING THE LEVEL  STANDARG TO BCL. X(S) OF STANDARG THE LEVEL  THE DEATH REPRESSOR ACTIVITY OF BCL. X(L), BUT NOT THAT OF BCL. X(S) OF STANDARG TO BCL. X(L), BUT NOT THAT OF BCL. X(S) OF STANDARG TO BCL. X(L), BUT NOT THAT OF BCL. X(S) OF STANDARG TO BC. X(S) OF ST	
HORVU ECOLI SALTY BORBU REOVJ HUMAN CLOAB PRVKA NEIMA NEIMA	ALIGNMENTS	uence update) otation updat leonent 6).  Craniata: Ver Catarrhini; H an S., Zhou H. BL/GenBank/Db BL/GenBank/Db BL/GenBank/Db THESE POTEI	
CCAT2_HORVU ACEK_ECOLI ACEK_SALTY RPSD_BORBU VSIS_REOVJ ADML_HUMAN HBD_CLOAB CELF_PRVKA OTCC_NEIMB RA51_SCHPO	ALI	STANDARD; PRT; 168 AA  1. 35, Last sequence update) 1. 40, Last sequence update) 1. 40, Last annotation updat 1. 22 BINDING COMPONENT 6). BCL2L8.  Uman).  .A.  A.  A.  A.  A.  ROMOTES CELL DEATH. SUCCESSF BCL-X(L) AND BCL-2, THEREBY IZATION OF BOTH THESE PROTEI BTATION OF BOTH THESE PROTEI TAY  A.I. OR BCL-X(S) (BY SIMILAR  IFLITY: EXPRESSED IN A WIDE CONTAINS A BCL-2 HOWOLOGY D CONTAINS A BCL-2 HOWOLOGY D BELONGS TO THE BCL-2 FAMILY	) 4
наненнаннан		Created) Last seq Last and NDING COM NDING COM NDING COM TIMATES; TIMATES; TO THE TERODIMER R BCL X (S R BC) X	
494 5784 631 1255 185 331 331 418		UMAN  V-1997 (Rel. 35, Created V-1997 (Rel. 35, Last se T-200 (Rel. 40, Last an ROTEIN (BCL-2 BINDING COR R BEC6 OR BCL2L8. Saptens (Human). Saptens (Human). Saptens (Human). TaxID=9606;	
355.77 335.77 34.8 34.8 34.8 34.8 34.8 34.8		AN STANDA  1997 (Rel. 35, 2000 (Rel. 40, 2000 (Rel.	,
4 4 4 4 W W W W W W W W W W W W W W W W	•	BAD_HWAN  BAD_HWAN  BAD_HWAN  BAD_HWAN  99234,  99234,  99254,  99254,  99254,  99254,  99254,  99254,  99254,  901-00v-1997 (Rel. 35, Last sequence update)  901-00r-2000 (Rel. 36, Last sequence update)  901-00r-2000 (Rel. 36, Last sequence update)  BAD PROTEIN (BCL-2 BINDING COMPONENT 6).  BAD PROTEIN (BCL-2 BINDING COMPONENT 6).  BAD OR BBC6 OR BCL2L8.  HOMM SAPLATO (Human).  NCB1_TaxID=9606,  [1]  SEQUENCE FROM N.A.  Yin D.X., Li 2., Huang B., Chen S., Zhou H.;  SEQUENCE FROM N.A.  Yin D.X., Li 2., Huang B., Chen S., Zhou H.;  SEQUENCE FROM N.A.  YIN D.X., Li 2., Huang B., Chen S., Zhou H.;  SEQUENCE FROM N.A.  YIN D.X., Li 2., Huang B., Chen S., Zhou H.;  SEQUENCE FROM N.A.  1- FUNCTION: PROMOTES CELL DEATH. BCL-X(L),  (RY SIMILARITY)  1- FUNCTION: PROMOTES CELL DEATH. BCL-X(L),  (RY SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMN-1-SIMILARITY: CONTAINS A BCL-2 FAMILY.  1- SIMILARITY: CONTAINS A BCL-2 FAMILY.  1- SIMILARITY: SHILONGS TO THE BCL-2 FAMILY.  1- SIMILARITY: CONTAINS A BCL-2 FAMILY.  1- SIMILARITY: SHILONGS TO THE BCL-2 FAMILY.  1- SIMILARITY: BLONGS TO THE BCL-2 FAMILY.  1- SIMILARITY: SHILONGS TO THE BCL-2 FAMILY.  1- SIMILARITY: BLONGS TO THE BCL-3 FAMILY.  1- SIMILARITY: BLONGS TO THE BCL-3 FAMILY.  1- SIMILARITY: BLONGS TO THE BCL-3 FAMILY.  1- SIMILARI	
888888844444 4986088644444 4990017849		RESULT 1 BAD_HUMAN 1D BAD_HUMAN 1D BAD_HUMAN 1D BAD_HUMAN 1D 101-007-1 01-007-1 02 BAD OR BI 03 BAD OR BI 05 BAD OR BI 06 BAD OR BI 07 BAD OR BI 08 BAD OR BI 09 BAD OR BI 00 BAD 00 CC	;
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01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last seq
01-OCT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 B'
57129 MW;
                                                                                                                                                                1 NLWAAQRYGRELRRMSDEFVD 21
                                                                                                                          42.48;
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                                                                                                                     Query Match
Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                 Bacteriophage rho-11s.
                                                                                                                                                                                                                                                                                                                  Lambda phage group.
NCBI_TaxID=10735;
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P09915:
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SEQUENCE
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F., "Genome structure of mycobacteriophage D29: implications for phage
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
204 AA
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 PRT;
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                                                                                                        (1)
SEQUENCE FROM N.A.
TISSUE-Brain, and Thymus;
MEDLINE-95136361; PubWed=7834748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Biol. 279:143-164(1998).
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22080 MW;
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Best Local Similarity 100.0
Matches 19; Conservative
STANDARD;
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                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                  204 AA;
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                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                 138
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                                                         OR BBC6
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O64206;
                                                                                                                                                                                                                                                                                                                                                                          Apoptosis.
BAD MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-87246516; PubMed-3109889;
Behrens B., Noyer-Weldner M., Pawlek B., Lauster R., Balganesh T.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Organization of multispecific DNA methyltransferases encoded by temperate Bacillus subtilis phages.";
EMBO J. 6:1137-1142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MODIFICATION METHYLASE RHOLISI (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
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-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE
S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
-!- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                          Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                     EMBL; AF022214; AAC18453.1; -. SEGUENCE 595 AA; 66397 MW; AFD123ED5371E263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y SIMILARITY.
AAAFB8FE01B8129E CRC64;
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PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
Transferase; Methyltransferase; Restriction system.
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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Pred. No. 5.
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HSSP: P05102; 5MHT.
REBASE; 2835; M.RhollsI.
InterPro; IPR001525; -.
Pfam; PF00145; DNA_methylase; 1.
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PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-60 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-72 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-85 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-98 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-111 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-124 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-137 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-136 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-136 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-176 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-176 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

AMIDATION (G-176 PROVIDE AMIDE GROUP).

PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=92225349; PubMed=1348717; MEDLINE=92225349; PubMed=1348717; Menaller M., Paravicini G., Egli C., Irniger S., Braus G.H.; Cloning, primary structure and regulation of the ARO4 gene, encoding the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                             AMIDATION (G-189 PROVIDE AMIDE GROUP).
PRROLIDONE CARBOXYLIC ACID (POTENTIAL).
AMIDATION (G-202 PROVIDE AMIDE GROUP).
PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).
PAMIDATION (G-212 PROVIDE AMIDE GROUP).
AMIDATION (G-228 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94078675; PubMed-8256522; Doignon F., Biteau N., Aigle M., Crouzet M.; The complete sequence of a 6794 bp segment located on the right arm of chromosome II of Saccharomyces cerevisiae. Finding of a putative dUTPase in a yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
90-MAY-2000 (Rel. 39, Last annotation update)
PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED
FEC 4.1.2.1.5) (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP
SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE).
ARCO OR YER249C OR YER1701.
Saccharomyces cerevisiae (Baker's yeast).
Saccharomyces cerevisiae (Baker's yeast).
Saccharomycetaies; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                              FDF1F52C47D4BB11 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.2%; Score 45;
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Matches 10; Conservative
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      Gene 113:67-74(1992).
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227
287 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
      RESULT 6
AROG_YEAST
ID AROG_YEAST
AC P32449;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Schmutzler C., Diekhoff D., Grimmelikhuijzen C.J.P.;
"The primary structure of the Pol-RFamide neuropeptide precursor protein from the hydromedusa Polyorchis penicillatus indicates a novel processing proteinase activity.";
Biochem. J. 299:431-436(1994).
                                                                                                                                                                                                                                                                                                        Polyorchis penicillatus (Hydromedusa).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Polyorchidae; Polyorchis.
NCBI_TaxID=6091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
                                                                     1;
                                   Length 503;
                                                                     Indels
                                      DB 1;
                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 18, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-LUL-1998 (Rel. 36, Last annotation update)
POL-RFAMIDE NEUROPEPTIDES PRECURSOR.
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                                 Score 46.5; DB Pred. No. 6.5; 4; Mismatches
                                                                                                                                                                                                                287 AA
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207 WSAQDIVGRRLREILEEYVD 226
                                   41.5%;
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                                                                                                 3 WAAQR-YGRELRRMSDEFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002544; -. Pfam; PF01581; FARP; 12. Neuropeptide; Amidation; SIGNAL
                                                                 Conservative
                                                                                                                                                                                                                STANDARD;
                                 Query Match
Best Local Similarity
Matches 10; Conserv
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P21259;
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NCBI_TaxID=9606;
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P35414;
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                                                                                  Aljinovic G., Pohl F.M., Pohl T.M.;
Submitted (Adg-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
                                                                                                                                                                                                                                                                   -i- ENZYME REGULATION: INHIBITED BY TYROSINE.
-i- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYMTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
-i- INDUCTION: BY AMINO ACID STARVATION.
-i- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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"The G protein-coupled receptor msr/APJ is expressed in endothelial
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-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                       ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).

CATALYTIC ACTIVITY: 7-PHOSPHO-2-DEHYDRO-3-DEOXY-D-ARABINO-HEPTONATE + ORTHOPHOSPHATE = PHOSPHOENOLPYRUVATE + D-ERYTHROSE 4-PHOSPHATE + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Aromatic amino acid biosynthesis; Lyase; Multigene family.
SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursors.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ORPHAN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-ocr-2000 (Rel. 40, Created)
01-ocr-2000 (Rel. 40, Last sequence update)
01-ocr-2000 (Rel. 40, Last annotation update)
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (MSR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NLWAAQRYGRELRRMSDE 18
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Yeast 9:1131-1137(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S38185; S38185
SGD; S0000453; ARO4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                  STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APJ_MOUSE
Q9WV08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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NAMES OF A PART 
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94124031; PubMed=8294032; O'Dowd B.F., Heiber M., Chan A., Heng H.H., Tsui L.-C., Kennedy J.L., Shi X., Petronis A., George S.R., Nguyen T.; Al Numan gene that shows identity with the gene encoding the angiotensin receptor is located on chromosome 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: ORPHAN RECEPTOR.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                            MGD; MGI:1346086, Agtril...
InterPro; IPR00276; --
Pfam; PF00001; 7tm_li...
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                        EMBL; AJ007612; CAB50696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LWAAQRYGRELRRMSDEFV 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95302501; Pubmed-7783207;
MEDLINE-95302501; Pubmed-7783207;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
The DNA sequence of equine herpesvirus 2.";
J. Mol. Biol. 249:520-528(1995)
-! CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
N PYROPHOSPHATE + DNA (N).
-! SUBCELLULAR LOCATION: NUCLEAR.
-! SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 45; DB 1; Length 380; 47.4%; Pred. No. 8.3;
    EMBL; AF100206; AAC72404.1; -.
InterPror; IPR000276; -.
Pfam; PF00001; 7tm_1; 1.
PRINYS; PR00237; GPRORHUDOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_ROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                  E84F03E31FABF7ED CRC64;
                                                                                                                                                                                 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Equine herpesvirus type 2 (strain 86/87) (EHV-2). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae. NCBI_TaxID-82831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                                                 6 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002064; -. Pfam; PF00136; DNA_pol_B; 1. PRINTS; PR00106; DNAPOLB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42606
                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 47.4 Matches 9; Conservative
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380 AA;
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52
67
92
101
145
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P52367;
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DOMAIN
TRANSMEM
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TRANSMEM
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CARBOHYD
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DPOL_HSVE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).

LLINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

78DB18BEA6D2B2E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSOLESPITED:
MATQUILES B.J., Hauer D.A., Clements J.E.;
"Identification and characterization of thirteen rhesus macaque chemokine receptors and chemokine receptor homologues.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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Pred. No. 8.3;
                                                                                                                                                               1 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                       PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
or send an email to license@isb-sib.ch).
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Macaca mulatta (Rhesus macaque).
                                                               InterPro; IPR000276; -.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                         42660 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                40.28;
                           EMBL; U03642; AAA18954.1; -. GCRDb; GCR_0806; -.
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                                                                                                                                                                                                                                                                                                                                                                                           380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                  27
52
67
67
101
126
1145
222
222
222
222
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                                          GCRDb; GCR_0
MIM; 600052;
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097666;
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TRANSMEM
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TRANSMEM
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Gaps

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8; Indels

370 AA

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STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=5476;
AROG CANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEDINE STRAIN-MASS DSM 3109; MEDLINE-99287316; PubMed=10360571; MEDLINE-99287316; PubMed=10360571; Melson M.L., Dodson R.J., Haft D.H., Hickey E.K., G. Mill S.H., Gain M.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Fratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from Mature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
-1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: 6-PHOSPHO-D-GLUCONO-1,5-LACTONE + H(2)0 = 6-PHOSPHO-D-GLUCONATE.
                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                              DB 1; Length 1008;
35;
                   Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Nuclear protein. SEQUENCE 1008 AA; 112664 MW; 252604AC9D03AB0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 399:323-329(1999).
-!- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 AA; 25325 MW; 9B0FD07EE01E60C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-WAY-2000 (Rel. 39, Last sequence update) 30-WAY-2000 (Rel. 39, Last annotation update) 6-PHOSPHOGLUCONOLACTONASE (EC 3.1.1.31) (6FGL).
                                                                                                                                              Score 44; DB 1
Pred. No. 35;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 9.4;
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PROSITE; PS00116; DNA_POLYMERASE_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga
                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001772; AAD36230.1; -.
                                                                                                                                              39.3%;
50.0%;
                                                                                                                                                                                                                                             1 NLWAAQRYG -- RELRRMSDEFV
                                                                                                                                         Query Match 39.39
Best Local Similarity 50.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ACEKYEREIRSATDOF 126
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGL OR DEVB OR TM1154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHOGLUCONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGR; TM1154;
                                                                                                                                                                                                                                                                                                                                                                                                                 6PGL_THEMA
Q9X0N8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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DD111D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the ARO4 gene encoding a second DAHP synthase.";

Curr Genet. 29:441-445(1995)

-!- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)

AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-

ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE FROM N.A. MEDLINE-96207468; PUPMed-8625423; Pereira S.A., Livi G.P., "Aromatic amino-acid biosynthesis in Candida albicans: identification "Aromatic amino-acid biosynthesis in Candida albicans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
-!- PATHWAX: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF ROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
-!- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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P41434;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 54.7 KDA PROTEIN IN IAPI-SOD INTERGENIC REGION (ORF15).
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dSDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED
EC 4.1.2.1.5) (PHOSPHO-2-EKETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP
SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: 7-PHOSPHO-2-DEHYDRO-3-DEOXY-D-ARABINO-
HEPTONATE + ORTHOPHOSPHATE = PHOSPHOENOLPYRUVATE + D-ERYTHROSE
4-PHOSPHATE + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001785; -.
Pfam; PF000793; DAHP_synth_1; 1.
Aromatic amino acid bosynthesis; Lyase; Multigene family SEQUENCE 370 AA; 40291 MW; 11E5E324C8D7B6DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 11651 / B792;
Sousa S., Pereira S.A., Livi G.P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U53216; AAB48240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||: |::::|| |
74 ALEYGKRLKKLADELKD 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
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AROG\_CANAL

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-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS
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WormPep; C54D1.5; CE06981.
InterPro; IPR000034; -.
InterPro; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              434
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513 LWLAARMGRDLR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LWAAQRYGRELR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       905 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                368
                                                                                                                                                                                                                        P31016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LML1_CAEEL
Q18823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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LML1_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-2000 (Rel. 40, Last annotation update)
TIGHT JUNCTION PROTEIN 20-3 (ZONA OCCLUDENS 3 PROTEIN) (TIGHT JUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence, genomic organization of the EcoRI-A fragment of Autographa
                                                                                                                                                                                                                                                                                                                                    VICOLOGY 191:1003-1008(1992).
--- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
--- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 294
--- ONWARD AND IS SHORTER (354 AA) DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                 MEDLINE-94303173; PubMed-8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                            californica nuclear polyhedrosis virus, and identification of a viral-encoded protein resembling the outer capsid protein VP8 of rotavirus.";
                                                                                                                                                                                                                    Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 262 AYYIRHWFA -> GTTLDTCLL (IN REF. 2)
463 AA; 54688 MW; D3643E87E2C6D373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 1;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L22858; AAA66660.1; -.
EMBL; M96361; AAA66798.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20069797; PubMed=10601346;
                                                                                                                                                                                             MEDLINE=93079853; PubMed=1333113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203_MOUSE STANDARD; F 090XY1; 01-0CT-2000 (Rel. 40, Last sequent of 1-0CT-2000 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 LWKA--YGRHLKLNSDECDD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.4%;
55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LWAAQRYGRELRRMSDEFVD 21
                                                                                             polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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TJP3 OR ZO3.
                                                                                                                                                                                                                                        Summers M.D.
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ID ZO3_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.4%; Score 43; DB 1; Length 905; 66.7%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minx P.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B787BA1592661FEE CRC64;
                                                                                                                                                                                                                                                                                                                        MGD: MGI:1310; IFBO
MGD: MGI:1310; IFBO
InterPro; IPRO01619; --
InterPro; IPRO01478; --
Pfam; PF00695; PDZ; 3.
PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
PROSITE; PS50106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LAMINIA-LIKE PROFEIN CS4D1.5 PRECURSOR.
C54D1.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tight junction; SH3 domain; Repeat; Membrane
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PDZ 2.
PDZ 3.
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LAMININ BGF-LIKE 1.
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LAMININ BGF-LIKE 3.
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1321 1321 N-LINKED (GLCNAC. . .) (POTENTIAL.) 1437 1437 N-LINKED (GLCNAC. . .) (POTENTIAL.) 1557 AA; 172723 MW; CAF0B51F8D5E8D2F CRC64;
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                                                                       Score 43; DB 1;
Pred. No. 82;
5; Mismatches
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                                                                        Query Match 38.4%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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1169 ASQKYGEQSKRMSE 1182
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ottilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G., Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.; J. Blol. Chem. 0:0-0(1997).
EMBL: AF021792; AAB72092.1; -.
EMBL; AF031523; AAB88124.1; -.
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SEQUENCE FROM N.A.
Takayama S., Reed J.C.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 2.4e-09;
Mismatches 0;
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01-JAN-1998 (TrEMBLrel. 05, Last sequenc
01-NOV-1998 (TrEMBLrel. 08, Last annotat
BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).
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Matches 21; Conserv
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070256 rattus norv
091hx1 rattus norv
0919n2 brachydanio
091843 mycobacteri
091403 pseudomonas
091y62 pseudomonas
091y62 pseudomonas
091y62 pseudomonas
09505 atrichum an
095001 homo sapien
09101 homo sapien
09101 coeccus
061125 burkholderi
091172 leishmania
04466 caenorhabdi
061172 leishmania
06465 arabidopsis
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59.892 Million cell updates/sec
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                                                                                                                                    ; Search time 46.39 Seconds
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                   425026 seqs, 132305027 residues
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Listing first 45 summaries
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141 NLWAAQRYGRELRRMSDEF 159
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HSU S.Y., HSUEL A.J.W.;
Interference of BAD (Bcl-xL/Bcl-2-associated death promoter) induced apoptosis in mammalian cells by 14-3-3 isoforms and Pll.";
MOI. Endocrinol. 11:1858-1867(1997).
EMBL; AF003523; AAC53374.1;
SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.; "Cloning and expression of the programmed cell death regulator Bad in the rat brain."; Neurosci. Lett. 243:137-140(1998).
                                                                                                                                    Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAD OR BAD-ALPHA.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.
"Functional characterization of two spilce variants of rat bad and
their interaction with bol-w in sympathetic neurons.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF03127; AAC15100.1;
EMBL; AF279910; AAF914271: -
SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-OCT-2000 (TrEMBLrel. 15, Last anno
                                    PRT;
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                                                                                                 BCL-2 ASSOCIATED DEATH PROMOTER,
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19, Conservative
                                    PRELIMINARY;
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                                                                                                                          Rattus norvegicus (Rat).
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TISSUE-BRAIN;
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                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Last annotation update)
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100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.100; Mismatches
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                                                                                               BCL-2 ASSOCIATED DEATH AGONIST BETA
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Cell Death Differ. 7:509-510(2000).
 PRT;
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NON_TER 1 1 SEQUENCE 95 AA: 10R04 AND
                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
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01-OCT-2000 (TrEMBLRE1. 15,
01-OCT-2000 (TREMBLRE1. 15,
01-MAR-2001 (TREMBLRE1. 16,
BAD (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NLWAAQRYGRELRRMSDEF 19
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.8
Matches 14; Conservative
 PRELIMINARY;
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RESULT Q10843

1 NLWAAQRYGRELRRMSDEF 19

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Gaps
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                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1248;
69;
   DB 2; Length 453;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE004720; AAG06332.1; -.
InterPro; IPR000049; -.
InterPro; IPR000408; -.
Prodom: PD003528; -; 1.
PR051TE; PS00626; RCC1_2; UNKNOWN_1.
SEQUENCE 1248 AA; 138499 WW; C3D3DBFEE6736C7A CRC64;
                                                                                                                                                                                                 Q9HZQ3;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
COBALAMIN BIOSYNTHETIC PROTEIN COBN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN PA3555.
                                  5;
                                                                                                                                                                           PRT; 1248 AA.
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 Score 49; DB 3
Pred. No. 23;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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 43.8%;
55.6%;
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                                                                   3 WAAQRYGR--ELRRMSDE 18
                                                                                      ||::| || |||::|
65 WASERQGREEELRRLASE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen."; Nature 406:959-964(2000).
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Best Local Similarity 50.0
Matches 11; Conservative
                                10; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                 COBN OR PA2944
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PAO1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9HY62
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Q9HY62
                                                                                                                                                   RESULT
Q9HZQ3
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tektaie F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Taylor K., Whitehead S., Barrell B.G., Squares S., Sqares R., Sulston J.E., Nature 393:537-544(1998).

Is SIMILARITY: TO M. PARAPUBERCULOSIS IS900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20(37337; PubMed-10984043; Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock-Wadnan S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 2; Length 223;
Pred. No. 2.6;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70456750017FEF37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 453 AA; 51539 MW; 1E7EA97E82EC5E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              091403 PRELIMINARY; PRT; 453 AA.
091403;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN PA1031.
             Q10843;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
11-NAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 24.1 KDA PROTEIN CY39.03C.
RV2014 OR MTCY39.03C.
 223 AA
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003346; -. Pfam; PF02371; Transposase_20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 223 AA; 24132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004535; AAG04420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.00,
                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NLWAAQRYGRELRRMSD 17
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculist: Rv2014:
                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=H37RV;
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                                                                                                                                                               NCBI_TaxID=1773;
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Q914U3
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InterPro;
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043521
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Wilkinson Support Calculated with Exact Probabilities: An Example Using Floricaula/LEAFY Amino Acid Sequences that Compares Three Using Floricaula/Lind Gene Gain/Loss in Seed Plants.";
Mol. Biol. Evol. 17:1914-1925(2000).

EMBL; AF286055; AAG42695.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Polytrichopsida;
Polytrichales; Polytrichaceae; Atrichum.
NCBI_TaxID=37310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAÎN=BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 339;
                                                                                                                                                                                                           Length 295;
                                                                                                                                                                                                                                                  Indels
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                                                                                                   EMBL; AE004776; AAG06943.1; -.
Hypothetical protein.
SEQUENCE 295 AA; 32919 MW; 5395218A63F6B360 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA.
                                                                                                                                                                                                           DB
28;
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                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                         Score 47;
Pred. No. 2
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                            120 VWSVQQLGEQIRRGSDCLAD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.0%;
61.1%;
                                                                                                                                                                                                                                                                                     2 LWAAQRYGRELRRMSDEFVD 21
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                                                                                                                                                                                                         42.0%;
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Best Local Similarity 61.1:
Matches 11; Conservative
                                                                                                                                                                                                         Query Match 42.0
Best Local Similarity 40.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atrichum angustatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11110908;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Gegers S.E., Richards S., Ashburner M., Hederson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Shbarg O., Chen L.X.,
RA Grown R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Obole C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayarkataroglu L., Beasley E.M.,
RA Beeson K.Y., Basno P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berry J.M., Cawley S., Dalhike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dalhike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dalhike C., Davenport L.B., Davies P.,
RA Dodson K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann R.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,
RA Horits N.C., Marvey D., Hehman T.J., Hernandez J.R., Hostin D., Houston K.A., Hehman T.J., Hernandez J.R., Hostin D., Houston K.A., Hehman T.J., Weinrandez J.R., Hostin D., Houston K.A., Lewitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Aluxi, Mattel B., Morintoh T.C., McLeod M.P., Moshrefi A.,
Mont S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralison D.R., Perdites W., Mobarry C., Morris J., Woshrefi A.,
Randert K., Remington K., Sauders R., Perdison D.K.,
Randert K., Wasarman D.A., Nixon K., Nixon R., Saith H.O.,
Randert K., Wasarman D.A., Wabarry C., Morris J., Wang X.,
Wang Z.-Y., Wasarman D.A., Wellschon M., Stung S., Zho X., Saith H.O.,
Randilams S.M., Woodage T., Worley K., Wu D., Yang S., Jao Q., Zheng L.,
Randilams S.M., Woodage T., Worley K., Wu D., Yang S., Jao Q., Zheng L.,
Randilams S.M., Woodage T., Worley K., Wu D., Yang S., Jao Q., Zheng C., Sheng C., Sheng C., Sheng C., Sheng S., Sheng S., Sheng S., Shen
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PERIPHERAL BLOOD, AND SPLEEN;
BDDLINE-B80904360;
O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
Cory S., Huang D.C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-our-1998 (TrEMBLrel. 06, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
BCL2-LIKE PROTEIN 11 (BCL2 INTERACTING MEDIATOR OF CELL DEATH).
BCL2L11 OR BIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ນ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4327F6726A98F524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.5; DB 5;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 NLWSALKYGYESVEREIVHVIDEDV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NLWAAQRYG----RELRRMSDEFV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulfatase; 1.
AA; 55063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSF; F13848; IFSU.
FlyBase; FBgn0036765; CG7408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interio,
Pfam; PF00884; Suir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     043522;
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Gaps

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Indels

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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 2; Length 574; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=1026B;
DeShazer D., Brett P.J., Woods D.E.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF064070; AAAD5463.1; -.
InterPro; IPR001173; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White S.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 AA; 64745 MW; 98F9936846491B25 CRC64;
                                                                                                                                                                                                                                                                                                                           (Pseudomonas pseudomallei)
                                                                                                                                                                                                                 (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02, Created)
02, Last sequence update)
14, Last annotation update)
                                                                                                                                                                                574 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     848 AA.
                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Last annot
PUTATIVE O-ANTIGEN METHYL TRANSFERASE.
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00535; Glycos_transf_2; 1.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94150718; Pubmed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.2%;
                                                                                                                                                                                                                                                                                                                       Burkholderia pseudomallei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94419
Q9419;
Q1-FEB-1997 (TrEMBLrel. 07
Q1-FEB-1997 (TrEMBLrel. 07
01-FEB-1997 (TrEMBLrel. 07
01-JUN-2000 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AAQRYGRELRRMSDEF 19
                                                                                                                                                                                  PRELIMINARY;
                                                                | ||:||: ||| |
283 YVREMRRVIDEFDD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                         8 YGRELRRMSDEFVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=28450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZK858.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                        01-AUG-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                069125
069125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                         RESULT 14
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q94419
                                                                                                                                                             069125
                                           ö
                                                                              q
                                                                                                                                                                                    δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                 -1- FUNCTION: INDUCES APOPTOSIS.
-1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
PROTEINS INCLUDING MCL-1, BCL-2XL, BFL-1, AND BHRP-1, DOES
PROTEINS INCLUDING MCL-1, BCL-2XL, BFL-1, AND BHRP-1, DOES
NOT HETERODIMENIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
BAX OR BARK (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOPLASMIC MEMBRANES
(BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; ISOFORM BIMEL (SHOWN HERE) AND
ISOFORM BIML; ARE PRODUCED BY ALTERNATIVE SPLICING: THE ISOFORMS
VARY IN CYTOTOXICITY WITH ISOFORM BIML BEING MORE POTENT THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=R1)
MEDLINE-2005896; PubMed=10567266;
MEDLINE-2005896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
"Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
EMBO J. 17:384-395(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus NCBI_TaxID-1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                           DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 2; Length 564; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 198;
                                                                                                                                                                                                                                                                       CYTOTOXICITY.
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
EMBL; AF032457; AAC39593.1; -.
EMBL; AF032458; AAC39594.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN ISOFORM BIML).
D75735E469CA6997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63667 MW; B8F50B9B0DFC8D51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
GLYCOSYL HYDROLASE, FAMILY 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB /
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR000712; -.
PROSITE; PS01259; BH3; FALSE_NEG.
Apoptosis; Alternative splicing; Membrane.
DOMAIN 148 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000461; -. Pfam; PF00128; alpha-amylase; 1. Hydrolase. S64 AA; 63667 MW; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 AA; 22171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.1%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001983; AAF10944.1;
HSSP; P21332; 1UOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LWAAQRYGRELRRMSDEF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radiodurans R1.
                                                                                                                                                                                                                                        ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; DR1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9RUK9;
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RESULT 13 Q9RUK9

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Gaps

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4.5
Compugen Ltd.
  GenCore version
Copyright (c) 1993 - 2000
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 protein search, using sw model OM protein 9, 2001, 15:54:03; Search time 28.81 Seconds October Run on:

(without alignments) 55.525 Million cell updates/sec

US-09-580-523-1\_COPY\_103\_123 Title: Perfect score:

1 NLWAAQRYGRELRRMSDEFVD 21 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* PIR 68:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

bad protein - mous hypothetical prote conserved hypothet cytochrome-c oxida cytochrome oxidase 3-oxoacyl- acyl-ca neuropeptide Pol-R angiotensin recept glycosyl hydrolase hypothetical prote gibberellin 2betaprobable threonine DNA polymerase rep site-specific DNA-hypothetical prote ACMNPV orf30 - Bom hypothetical prote hypothetical prote deoxyribodipyrimid cobalamin biosynth gp13 protein - Myc conserved hypothet 2-dehydro-3-deoxyp oxidoreductase, so Acorf-30 protein ribosome recycling probable cytochrom trigger factor [va site-specific DNA Description SUMMARIES A55671 D70760 E83517 G83278 B72801 F83201 CTBPRH S43852 S38185 I38435 H75403 T28055 T52577 A96753 S55603 JQ1019 C81868 F72289 A64538 H71969 H69829 F72853 T41775 T28811 Match Length DB 202 432 432 461 Score 47.5 47.5 46.5 43.5 Result ٠ ي 

threonine synthase	proprotein convert	alpha,alpha-trehal	myosin V - fruit f	70K heat shock cha	hypothetical prote	probable cytochrom	cytochrome c oxida	hypothetical prote	hypothetical prote	probable monooxyge	hypothetical prote	conserved hypothet	hypothetical prote	protein kinase C h	membrane transport	
T08545	KXRTC1	T05860	T13939	T44956	T25773	B83452	E82200	T12515	T22799	D64801	G85566	A82827	F85356	T33400	T40297	
7	<del>, -</del> 1	~	7	~	7	7	N	7	7	Н	7	7	7	7	~	
526	752	795	1792	69	166	203	206	352	388	391	391	395	447	267	217	
37.5	37.5	37.5	37.1	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.6	
42	42	42	41.5	41	41	41	41	41	41	41	41	41	41	41	41	
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

bad protein - mouse

C; Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C; Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999
C; Accession: A55671
R; Yang, E: Zha, J: Jockel, J: Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A; Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot A; Reference number: A55671; MUID:95136361
A; Accession: A55671
A; Accession: A5671
A; Accession: A55671
A; Accession: A5671
A; Ac

Gaps ö Length 204; 91.1%; Score 102; DB 2; 100.0%; Pred. No. 1.8e-08; ive 0; Mismatches 0; Query Match 91.1 Best Local Similarity 100. Matches 19; Conservative

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## 1 NLWAAQRYGRELRRMSDEF 19 δλ

140 NLWAAQRYGRELRRMSDEF 158 qq

hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999
C; Accession: D70706
R; Color, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature: 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUD:98295987
A; Accession: D70760
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-223 <COL>
A; Residues: 1-223 <COL>
A; Residues: 1-223 <COL>
A; Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:e12999
A; Experimental source: strain H37Rv

A; Gene: Rv2014

Length 223; Score 53; DB 2; Pred. No. 0.83; 47.3%; 58.8%; Query Match Best Local Similarity

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A; Accession: F83201
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-295 <STO>
A; Cross-references: GB: AE004776; GB: AE004091; NID: 99949701; PIDN: AAG06943.1; GSPDB:GN
A; Experimental source: strain PAO1
C; Genetics:
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(C;Accession: A28137
(C;Accessi
                                                                  C. Accession: B72801
R. Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 29, 143-164, 1998
A. Title: Genome structure of mycobacteriophage D29: Implications for phage evolution. A; Reference number: A72800; MuID:98300335
A. Accession: B72801
A. Status: preliminary
A. Molecule type: DNA
A; Residues: 1-595 <FOR>
A; Cossreferences: GB: AF022214; NID:93172250; PIDN: AAC18453.1; PID:93172260
C; Genetics:
A; Gene: 13
C; Superfamily: Mycobacterium phage L5 gene 13 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein PA3555 [imported] - Pseudomonas aeruginosa (strain PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Clson, M.V.
Nature 406, 959-964, 2000
C;Species: Mycobacterium phage D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83201
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 24-Oct-1997
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C;Superfamily: Escherichia coli hypothetical protein b2256
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Pred. No. 9.4;
5; Mismatches
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ilarity 40.0%;
Conservative
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Best Local Similarity 47.6%;
Matches 10; Conservative
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Best Local Similarity
Matches 8; Conserv
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K.; Lim,
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A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: DNA
A; Status: 1-1248
A; Status: 1-1248
A; Residues: 1-1248
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A; Cross-references: Strain PAO1
C; Genetics: A; Genetics: A; Genetics: A; Genetics: Coby; PA2944
C; Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
A;Accession: E83517
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A;Status: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-453 <STO>
A;Cross-references: GB:AE004535; GB:AE004091; NID:g9946936; PIDN:AAG04420.1; GSPDB:GN001
A;Cross-references: strain PA01
C;Genetics:
A;Gene: PA1031
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C:Species: C:Species: Pseudomonas aeruginosa
C:Species: C:Species: Pseudomonas aeruginosa
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A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA01)
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A.; Larbig,
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C;Date: 15-5ep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83517
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb
Nature 406, 959-964, 2000
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Pred. No. 19;
4; Mismatches
Mismatches
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Pred. No.
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B72801
gpl3 protein - Mycobacterium phage D29
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Best Local Similarity 50.0%;
Matches 11; Conservative
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ilarity 55.6%;
Conservative
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                                                                                    1 NLWAAQRYGRELRRMSD 17
Conservative
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A; Reference number: $45906
A; Recession: $46126
A; Accession: $46126
A; Recidues: 1-370 < ALJ>
A; Residues: BMBL: 236118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR2
R; Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
Submitted to the Protein Sequence Database, August 1994
A; Reference number: $45940
A; Accession: $46130
A; Molecule type: DNA
A; Residues: 1-370 < ALD
A; Toross-references: EMBL: 236118; NID: 9536664; PIDN: CAA85212.1; PID: 9536665; MIPS: YBR2
R; Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.
A; Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr
A; Accession: JN0322; MUID: 92225349
                                                                                                                                                                                                                                                                                C; Species: Saccharomyces cerevisiae
C; Date: 31-Dec-1993 #text_change 22-Jun-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C; Date: 31-Dec-1993 #sequence I will Aigle, M.; Crouzet, M.
Yeast 9, 1131-1137, 1993
A; Title: The complete sequence of a 6794 bp segment located on the right arm of chrom A; Reference number: S38185; MUID:94078675
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A; Molecule.type: DNA
A; Molecule.type: DNA
A; Molecule.type: DNA
A; Molecule.type: DNA
A; Cross-references: 352-370 (KU2>
A; Cross-references: GB:X61107
C; Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
C; Genetics:
C; Genetics:
A; Gene: SGD:ARO4
A; Cross-references: SGD:S0000453; MIPS:YBR249c
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                                                                                                                                                                                                                             2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces N; Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DAHP synthas
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Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-370 c DOI>
A; Cross-references: GB: L20296; NID: 9311101; PIDN: AAA65607.1; PID: 9311102
B; Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A;Residues: 1-204,208-370 <KUE>
A;Cross-references: EMBL:X61107
A;Cross-references: EMBL:X61107
B;Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.
J. Bacteriol. 175, 5548-5558, 1993
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C; Function:
A; Description: aldehyde-lyase; carbon-carbon lyase
A; Dathway: aromatic amino acid biosynthesis; shikimate pathway
A; Note: first step in shikimate pathway
C; Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C; Keywords: aldehyde-lyase; aromatic amino acid blosynthesis; c
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24;
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Pred. No.
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50.0%;
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Best Local Similarity 50.u.
                             1 NLWAAQRYGREL
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R;Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Spencer, A.N.
Biochem. Blophys. Res. Commun. 183, 375-382, 1992
A;Title: Isolation of the neuropeptide <Glu-Trp-Leu-Lys-Gly-Arg-Phe-NH2 (PolRFamide II)
A;Reference number: JQ2216; MUID:92198411
A;Accession: JQ2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Isolation of <Glu-Leu-Gly-Gly-Arg-Phe-NH-2(Pol-RFamide), a novel neuropepti
A;Reference number: A30321; MUID:89105774
A;Accession: A30321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuropeptide Pol-RFamide precursor - hydromedusa (Polyorchis penicillatus)
N;Contains: neuropeptide Pol-RFamide I; neuropeptide Pol-RFamide II
C;Species: Polyorchis penicillatus
C;Species: Polyorchis penicillatus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: S43852; JQ22L6; A30321
R;Schmutzler, C.; Dlekhoff, D.; Grimmelikhuijzen, C.J.P.
R;Schmutzler, C.; Dlekhoff, D.; Grimmelikhuijzen, C.J.P.
A;Title: The primary structure of the Pol-RFamide neuropeptide precursor protein from the Reference number: S43852; MUID:94226606
A;Accession: S43852
                       R; Trautner, T.A.
submitted to the EMBL Data Library, September 1987
A; Reference number: A94502
A; Contents: annotation: revision of residue 476
C; Comment: This enzyme methylates cytosine within the sequences GGCC and GACCTC.
C; Superfamily: site: Specific methyltransferase (cytosine-specific) EcoRII
C; Reywords: methyltransferase; S-adenosylmethionine
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R;Grimmelikhuijzen, C.J.P.; Hahn, M.; Rinehart, K.L.; Spencer, A.N.
Brain Res. 475, 198-203, 1988
                                                                                                                                                                                                                                                                                      Length 503;
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Pred. No. 19;
4; Mismatches
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Pred. No. 19;
5; Mismatches
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50.0%; Pre
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207 WSAQDIVGRRIREILEEYVD 226
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A; Cross-references: EMBL: X05242
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Best Local Similarity 50.0
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-287 <SCH>
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Gaps

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gibberellin 2beta-dioxygenase (EC 1.14.11.13) 3 [validated] - Arabidopsis thaliana N;Alternate names: gibberellin 2-oxygenase: giberellin 2beta-dioxygenase (EC 1.14.11. C;Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 24-oct-2000 #sequence_revision 24-oct-2000 #text_change 02-Feb-2001 C;Accession: T55577; A84758 F:Thomas, S.G.; Phillips, A.L.; Hedden, P. Proc. Natl. Acad. Sci. U.S.A. 96, 4698-4703, 1999 A;Title: Molecular cloning and functional expression of gibberellin 2-oxidases, multi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: EMBL:279759; PIDN:CAB02138.1; GSPDB:GN00019; CESP:2K858.1 A)Experimental source: clone ZK858 C; Genetics: A;Genetics: A;Gene: CESP:ZK858.1 A;Gene: CESP:ZK858.1 A;Gene: 2659:ZK858.1 A;Hap position: 1 A;Introns: 26/3; 82/3; 130/3; 195/3; 241/3; 613/1; 762/1
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probable threonine synthase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C;Reywords: oxidoreductase
                                            A;Accession: T28055
A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, September 1996
A;Reference number: 220462
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Pred. No. 55;
5; Mismatches
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Pred. No.
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Best Local Similarity 36.8%;
Matches 7; Conservative
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38.9%;
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A;Cross-references: EMBL:279759;
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43 WRRKRYGLNIQGLHEEIVD 61
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136 AVEEYIKEMKRMSSKFLE 153
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Best Local Similarity 38.9.
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A; Map position: 2
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                                                                                          A; Molecule type: DNA
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W. Shalte, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A; Reference number: A75250; MUID: 20036896
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-564 <WHI>
A;Cross-references: GB:AE001983; GB:AE000513; NID:g6459123; PIDN:AAF10944.1; PID:g645912
                                                                                                                                                          C;Accession: I38435
R;O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
                                                                                                                                                                                                                                 A;Title: A human gene that shows identity with the gene encoding the angiotensin receptor A;Reference number: 138435; MUID:94124031
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28055
R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                C;Species: Homo sapiens (man)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                             A;Accession: I38435
A;Status: preliminary
A;Adcolecule type: DNA
A;Residues: 1-380 <RES>
C;Genetics: EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425352
C;Genetics:
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C;Superfamily: alpha-glucosidase; alpha-amylase core homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 2
Pred. No. 25;
2; Mismatches
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Pred. No. 37;
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                                                                                             angiotensin receptor homolog APJ - human
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 11q12
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.2%;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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283 YVREMRRVIDEFDD 296
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Best Local Similarity
Matches 9; Conserv
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C; Accession: A96753

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, X.; Liu, Z.X.; Li, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID: 21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1008 A;Tessidues: 1-1008 CTELD
A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13796.1; PID:g695181
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C;Superfamily: herpesvirus DNA-directed DNA polymerase
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A;Motacule type: DNA
A;Rosidues: 1-516 <STO>
A;Cross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141
C;Genetics:
A;Gene: F3N23.1
A;Map position: 1
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C;Date: 27-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C;Date: 27-Oct.1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C;Accession: S55603
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S5594; MUID:95302501
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Pred. No. 48;
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DNA polymerase replicative chain - equine herpesvirus 2
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Pred. No. 94;
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50.0%;
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Best Local Similarity 50.0 Matches 11; Conservative
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1, Appli 2, Appli 6, Appli 13, Appl 13, Appli 4, Appli 17, Appli 4, Appli 4, Appli 4, Appli

Sequence

sequence 1, Ap Sequence 2, Ap Sequence 13, A Sequence 13, A Sequence 13, A Sequence 17, A Sequence 17, A Sequence 17, A Sequence 4, Ap Sequence 4, Ap Sequence 26, A Sequence 26, A

Sequence

Run on:

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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
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GENERAL I
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99.4%; Pred. No. 2.1e-84;
ive 1; Mismatches 0;
US-08-455-543A-47
US-08-223-305C-47
US-08-227-420-1
US-08-922-865-2
US-08-986-217-6
US-08-986-217-6
US-08-986-217-6
US-08-986-217-6
US-08-986-217-6
US-08-331-565-17
US-09-321-479-17
US-09-227-420-4
US-09-227-420-4
US-08-661-479-26
US-08-661-479-26
US-08-93-565-26
US-08-661-479-26
US-08-908-737-2
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; Patent No. 5965703
; GENERAL INFORMATION:
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Matches 167; Conserv
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1 MFQIPEFEPSEQEDSSSAER......RVFQSWWDRNLGRGSSAPSQ
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-733-505A-12
US-08-733-505A-13
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                  121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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                                                                                                                                                                               Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tue, Henry
APPLICANT: Corley, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 902; DB 3; L4
Pred. No. 2.1e-84;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 168 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.4
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 2194304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                   US-08-985-335-1
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US-08-985-335-1
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54 QPTSSSHHGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene and Protein for Regulation of Cell Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 LRRMADEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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Pred. No. 9e-69;
                                                                                                                                                                             ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLIFERATION
                                   Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INFORTION:
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08985335 Patent No. 6080847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Colley, well C.
TITLE OF INVENTION: PROTEINS AS
TITLE OF INVENTION: PROLIFERATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 166 amino acids TYPE: amino acid
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ADDRESSEE: Saliwanch
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Best Local Similarity
Matches 146; Conserv
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                                                                                                                                                                                                                                                   Florida
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; MOLECULE TYPE:
US-08-665-617-2
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                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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RESULT 3
US-08-665-617-2
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STATE:
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 71.4%; Score 646; DB 1; Length 204; Best Local Similarity 75.0%; Pred. No. 2.7e-58; Matches 126; Conservative 13; Mismatches 23; Indels
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Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BG1-x/BG1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILLIG DATE: 31.OCT-1994
CLASSIFICATION: 435
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APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1572(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFRA: (415) 326-2420
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acids
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TOPOLOGY: linear
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LOCATION: 1..204
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APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl.x/Bcl.2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTES for Windows Version 2.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATHOR DATE:
ATHORNOMEN.
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Pred. No. 4.7e-68;
1; Mismatches 25
                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0421 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORREY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGIETRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08333565
Patent No. 5622852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.9%;
Best Local Similarity 84.5%;
Matches 142; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650-845-4166
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linear
          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1683637
                                                                                                         STREET: 31/4 ru.
                                                                                                                                                                                                                      USA
                                                                                                                                                                              STATE: CA
COUNTRY: US
ZIP: 94304
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LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1
            SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HGCAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNIMAAQRYGRELRRMSDE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT ENTRY STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 204;
                                                                                                                                                                                                                                                                                                                                                              /note= "Deduced amino acid sequence of mouse BAD."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/733,505A FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 646; DB 2; 75.0%; Pred. No. 2.7e-58; tive 13; Mismatches 23.
                                                                                     15726A-000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIJONAGA, TOURNELLAND, DONALD R.
REGISCHRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
PILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WIlliam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726
TELECOMMUNICATION INFORMATION:
TELEFAN (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.45
Best Local Similarity 75.05
Matches 126; Conservative
                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
TELEFAX: (
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1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                      Gaps
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Olteradorf, Tilman
APPLICANT: Olteradorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
TITLE OF INVENTION: Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
71.4%; Score 646; DB 2; Length 204; ilarity 75.0%; Pred. No. 2.7e-58; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 645; DB 2; Length 204;
; Pred. No. 3.4e-58;
12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                      121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CULF: >112.
CULF: >112.
CULF: >112.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1D 1929
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-717-123-3; Sequence 3, Application US/08717123; Patent No. 5965703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.3%;
75.0%;
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amino acid
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71.3%
Best Local Similarity 75.0%
Matches 126; Conservative
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MOLECULE TYPE: peptide
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CLASSIFICATION: 530
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                       STREET: 7733 FOR CITY: ST. LOUIS STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                           63105
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                                                              98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMTDE 157
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                                                                                                                                                                                                                                                                         Sequence 12, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL.XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.0%; Score 643; DB 2; Length 204; Best Local Similarity 74.4%; Pred. No. 5.4e-58; Matches 125; Conservative 14; Mismatches 23; Indels
                                                                                                                                                   158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
                                                                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEPHONE: (314) 727-5188
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 13, Application US/08733505A
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MOLECULE TYPE: peptide
US-08-733-505A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 7733 FORE
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRAAPPNLWAAQRYGRELRRMSDE 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: RORSMEER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.0%; Score 643; DB 2; Best Local Similarity 74.4%; Pred. No. 5.4e-58; Matches 125; Conservative 14; Mismatches 23.
                                                                                                                                                     ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (314) 727-5188
TELEFAX: (344) 727-6092
INFORMATION FOR SEQ ID 0: 13:
SEQUENCE CHARACTERISTICS:
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Gaps

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63 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADEF 121
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                                                                                                                                                                                                                                         34.4%; Score 311; DB 2; L 98.3%; Pred. No. 5.7e-25; tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,197
ER: 965458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 95.197
REFERENCE/DOCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.0%;
96.6%;
        (314) 727-6092
  TELEFAX: (314) 727-609.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.33
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.08
Best Local Similarity 96.68
Matches 57; Conservative
                                              SEQUENCE CHARACTERISTICS:
                                                                      59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 59 amino acids
                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide US-08-733-505A-56
                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                              STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-733-505A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-733-505A-57
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                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-733-505A-55

Sequence 55, Application US/08733505A

Patent No. 5856445;
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED WUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF EXQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.7%; Score 640; DB 2; 73.8%; Pred. No. 1.1e-57; ive 15; Mismatches 23;
                                                                                                                                                                                                                                       965458
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/POCKET NUMBER: 9654:
TELECOMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFRAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 35,197 REFERENCE/DOCKET NUMBER: 96. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 73.88
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-733-505A-14
                                                                                                                                                   CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS: 0; Score 308; DB 2; Length 59; Pred. No. 1.1e-24; 2; Mismatches 0; Indels ZIP: 054105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Rolease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400 CITY: ST. LOUIS STATE: MISSOURI

CLASSIFICATION: 530

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Fatent No. 5856445
GENERAL INPORMETION:
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL.-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
TITLE OF INVENTION BCL.-XL/BCL-2 ASSOCIATED CELL DEATH BCL.-XL/BCL-2 ASSOCIATED CELL DEATH BCL.-XL/BCL-2 ASSOCIATED CELL DEATH BCL.-XL/BCL-2 ASSOCIATED CELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRAAPPNLWAAQRYGRELRRMSDEF 59
Sequence 57, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: RORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL.*XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 308; DB 2; Length 59;
Pred. No. 1.1e-24;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICALLO...
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/ACENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 95.197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
TELEFAX: (314) 727-6092
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.0%;
96.6%;
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Best Local Similarity 96.6°
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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SEQUENCE CHARACTERISTICS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4370 La
CITY: San Diego
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-717-123-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KORSHEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: G.
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
9
                                                                                                                                                                                                                                                                                                                                                                                  71.4%; Score 646; DB 2; Length 204; 75.0%; Pred. No. 2.7e-58; tive 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                     /note= "Deduced amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE JOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEFRAM: (415) 326-2400
TELEFRAM: (415) 326-2400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                     of mouse BAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08733505A
Patent No. 5856445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96
RECOMMUNICATION INFORMATION:
                                                                                                                                                             LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0%
Matches 126; Conservative
                                                                                                                                                                                                   single
                                                                                                                                                                                                                              MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                ) CTHER INFORMATION:

) OTHER INFORMATION:

US-08-661-479-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                              NAME/KEY: Protein
                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 7733 FORGETY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEPHONE:
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                                                                                                                                                                                                                                                                                                                          1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Horne, William A. APPLICANT: Oltersdorf, Tilman TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 Length 204;
                                                                                                                                                                                                                                                                                                                                                                                121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patent PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATONEX/AGENT INPORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERRNCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                           ;; Score 646; DB 2;
;; Pred. No. 2.7e-58;
13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.3%; Score 645; DB 2;
75.0%; Pred. No. 3.4e-58;
tive 12; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-717-123-3
; Sequence 3, Application US/08717123
; Patent No. 5965703
                                                                                                                                                       71.4%;
75.0%;
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 535-9001
TELERAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     Best Local Similarity 75.08
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 amino acids
                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/POCKET NUMBER: 9654
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID 0: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 204 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide US-08-733-505A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                  ADDARD 7/22 CITY: ST. LOUIS
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Best Local Similarity
                         GENERAL INFORMATION:
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                                        61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAORYGRELRRMADE 120
                                                             98 HGGAGAMETRSRHSSYPAGTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMTDE 157
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  97
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43 MFQIPEFEPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KORSHEYER, STANLEY J.
APPLICANT: KORSHEYER, STANLEY J.
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                       121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                          158 FEGSF-KGLPRPKSAGTATQMRQSAGWTRIIQSWWDRNLGKGGSTPSQ 204
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.0%; Score 643; DB 2;
1larity 74.4%; Pred. No. 5.4e-58;
Conservative 14; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                        STREET: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPTIFEE
                                                                                                                                                                                                                                                                 Sequence 12, Application US/08733505A
Patent No. 5856445
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US-08-733-505A-13
: Sequence 13, Application US/08733505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATORNEY/ACENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9654
TELECOMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-692
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 204 amino acids
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MOLECULE TYPE: peptide
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Matches 125; Conserv
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61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
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TITLE OF INVENTION: SREINE SUBSTITUTED MUTANTS OF TITLE OF INVENTION: SREINE SUBSTITUTED MUTANTS OF TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSE: HOWELL F. ...
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US-08-733-505A-14

Sequence 14, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.0%; Score 643; DB 2; 74.4%; Pred. No. 5.4e-58; tive 14; Mismatches 23
                                                                                                                                                                                                                          E: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BLVD., SUITE 1400
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STREET: 7733 FORSYTH BLVD., SUITE 1400
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

October 9, 2001, 15:58:34; Search time 18.99 Seconds (without alignments) 182.158 Million cell updates/sec Run on:

09-580523-1B 905 Title: Perfect score:

1 MFQIPEFEPSEQEDSSSAER....,RVFQSWWDRNLGRGSSAPSQ 168 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

197339 Total number of hits satisfying chosen parameters:

197339 seqs, 20590346 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

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5: /cgn2\_6/ptcdata/2/jaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptcdata/2/jaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appl							Appl	Appl	Appli	Appli	Appli	App1i	Appl	Appl	Appli	Appli
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sedneuce	Sequence	Sequence	Sequence	Sequence	Sequence
US-08-717-123-2	US-08-985-335-1	US-08-665-617-2	US-08-985-335-7	US-08-333-565-2	US-08-661-479-2	US-08-733-505A-1	US-08-717-123-3	US-08-733-505A-12	US-08-733-505A-13	US-08-733-505A-14	US-08-733-505A-55	US-08-733-505A-56	US-08-733-505A-57	US-08-733-505A-58	US-08-333-565-10	US-08-661-479-10	US-08-149-097D-35	US-09-041-886-21	US-09-026-587-3	US-09-227-420-3	US-08-337-602-3	US-08-558-135-3	US-08-455-543A-48	US-08-223-305C-48	US-08-713-118-2	US-09-452-007-2
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168	168	166	168	204	204	204	204	204	204	7			59	59	23	23	2509	1182	393	393	434	434	2237	2237	2337	2337
99.7	99.7	82.7	81.9	71.4	71.4	71.4	71.3	71.0	71.0	7.07	34.4	34.0	34.0	33.7	12.5	12.5	10.7	10.7	10.0	٠.				6.6		6.6
902	902	748	741	646	646	. 646	645	643	643	640	311	308	308	305	113	113	97	96.5	90.5	90.5	06	06	06	06	90	90
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81.9 168 3 US-08-985-335-7 Sequence 7, 71.4 204 1 US-08-661-479-2 Sequence 2, 71.4 204 2 US-08-61-479-2 Sequence 2, 71.4 204 2 US-08-733-5058-1 Sequence 2, 71.4 204 2 US-08-733-5058-1	99.7 168 2 US-08-717-123-2 Sequence 2, 99.7 168 3 US-08-985-335-1 Sequence 2, 82.7 166 1 US-08-965-617-2 Sequence 2, 81.9 168 3 US-08-965-5135-7 Sequence 2, 71.4 204 1 US-08-333-565-2 Sequence 2, 71.4 204 2 US-08-661-479-2 Sequence 2, 71.3 204 2 US-08-717-123-3 Sequence 2, 71.3 204 2 US-08-717-123-3 Sequence 3, 71.3 204 2 US-08-717-123-3	99.7 168 2 US-00-717-123-2 Sequence 2, A 99.7 168 3 US-08-985-335-1 Sequence 1, A 82.7 166 1 US-08-665-617-2 Sequence 2, A 81.9 168 3 US-08-985-335-7 Sequence 2, A 71.4 204 1 US-08-333-565-2 Sequence 2, A 71.4 204 2 US-08-661-479-2 Sequence 2, A 71.3 204 2 US-08-717-123-3 Sequence 1, A 71.3 204 2 US-08-717-123-3 Sequence 3, A 71.0 204 2 US-08-733-505A-12 Sequence 1, A 71.0 204 2 US-08-733-505A-12 Sequence 1, A 71.0 204 2 US-08-733-505A-12 Sequence 1, A 71.0 204 2 US-08-733-505A-12 Sequence 12, A 71.0 204 2 US-08-73-505A-12 Sequence 12, A 205 2 US-08-73-505A-12 Sequence 12, A 205 2 US-08-73-505A-12 Seque	99.7 168 2 US-08-717-123-2 Sequence 2, A 99.7 168 3 US-08-985-335-1 Sequence 1, A 82.7 168 3 US-08-985-335-1 Sequence 2, A 81.9 168 3 US-08-985-335-7 Sequence 2, A 81.9 105-08-333-565-2 Sequence 2, A 71.4 204 2 US-08-661-479-2 Sequence 2, A 71.4 204 2 US-08-733-505A-1 Sequence 1, A 71.3 204 2 US-08-733-505A-1 Sequence 1, A 71.0 204 2 US-08-733-505A-12 Sequence 12, 71.0 204 2 US-08-733-505A-13 Sequence 12,	99.7 168 2 US-08-717-123-2 Sequence 2, A 882.7 168 3 US-08-985-335-1 Sequence 2, A 882.7 166 1 US-08-985-335-7 Sequence 2, A 81.9 168 3 US-08-985-335-7 Sequence 7, A 71.4 204 1 US-08-985-335-7 Sequence 7, A 71.4 204 2 US-08-733-565-2 Sequence 2, A 71.4 204 2 US-08-733-505A-1 Sequence 1, A 71.0 204 2 US-08-733-505A-12 Sequence 1, A 70.7 204 2 US-08-733-505A-13 Sequence 12, 70.7 204 2 US-08-733-505A-14 Sequence 13, 70.7 204 2 US-08-733-505A-14 Sequence 13, 70.7 204 2 US-08-733-505A-14 Sequence 13, 70.7 204 2 US-08-733-505A-14 Sequence 14, 70.7 2 US-08-733-705A-14 Sequence 14, 70.7 2 US-08-733-705A-14 Sequence 14, 70.7 2 US-08-733-705A-1	99.7 168 2 US-08-717-123-2 Sequence 2, A 99.7 168 3 US-08-985-335-1 Sequence 1, A 82.7 168 3 US-08-985-335-1 Sequence 1, A 82.7 166 1 US-08-665-617-2 Sequence 2, A 81.9 168 3 US-08-985-335-7 Sequence 2, A 71.4 204 1 US-08-333-565-2 Sequence 2, A 71.4 204 2 US-08-661-479-2 Sequence 2, A 71.3 204 2 US-08-717-123-3 Sequence 3, A 71.0 204 2 US-08-717-123-3 Sequence 1, A 71.0 204 2 US-08-713-505A-13 Sequence 13, 71.0 204 2 US-08-713-505A-13 Sequence 13, 71.0 204 2 US-08-713-505A-14 Sequence 54, 34.4 59 2 US-08-733-505A-14 Sequence 55,	99.7 168 2 US-08-717-123-2 Sequence 2, A 99.7 168 3 US-08-985-335-1 Sequence 1, A 20.8 168 3 US-08-985-335-1 Sequence 1, A 20.8 1 US-08-985-335-7 Sequence 2, A 20.8 2 US-08-985-335-7 Sequence 2, A 71.4 20.4 2 US-08-333-565-2 Sequence 2, A 71.4 20.4 2 US-08-33-565-1 Sequence 2, A 71.3 20.4 2 US-08-717-123-3 Sequence 2, A 71.0 20.4 2 US-08-733-505A-12 Sequence 12, 71.0 20.4 2 US-08-733-505A-13 Sequence 13, 70.7 20.4 2 US-08-733-505A-14 Sequence 13, 34.4 59 2 US-08-733-505A-55 Sequence 55, 34.0 59 2 US-08-733-505A-55 Sequence 55, 34.0 59 2 US-08-733-505A-55 Sequence 55, 35 US-08-733-505A-55 Sequence 56, 35 US-08-733-505A-56 Sequence 56, 35 US-08-7	99.7 168 2 US-08-717-123-2 Sequence 2, A 882.7 168 3 US-08-985-335-1 Sequence 2, A 882.7 166 1 US-08-985-335-1 Sequence 2, A 882.7 166 1 US-08-985-335-7 Sequence 7, A 71.4 204 1 US-08-985-335-7 Sequence 7, A 71.4 204 2 US-08-985-335-7 Sequence 7, A 71.4 204 2 US-08-733-565-2 Sequence 2, A 71.3 204 2 US-08-733-565-1 Sequence 1, A 71.0 204 2 US-08-733-505A-12 Sequence 12, 71.0 204 2 US-08-733-505A-14 Sequence 13, 70.7 204 2 US-08-733-505A-14 Sequence 14, 70.7 204 2 US-08-733-505A-15 Sequence 15, 34.4 59 2 US-08-733-505A-56 Sequence 55, 34.0 59 2 US-08-733-505A-57 Sequence 57, 34.0 59 2 US-08-733-505A-57 Se	99.7 168 2 US-08-717-123-2 Sequence 2, A B 2.7 168 3 US-08-985-335-1 Sequence 1, A B 2.7 166 1 US-08-985-335-1 Sequence 2, A B 2.7 166 1 US-08-985-335-7 Sequence 2, A Sequence 2, A 14.4 204 1 US-08-333-565-2 Sequence 2, A 14.4 204 2 US-08-985-335-7 Sequence 2, A 14.4 204 2 US-08-661-479-2 Sequence 2, A 14.3 204 2 US-08-717-123-3 Sequence 3, A 14.4 204 2 US-08-733-505A-13 Sequence 12, A 14.4 59 2 US-08-733-505A-14 Sequence 13, A 14.4 59 2 US-08-733-505A-56 Sequence 55, 34.0 59 2 US-08-733-505A-56 Sequence 56, 34.0 59 2 US-08-733-505A-56 Sequence 56, 34.0 59 2 US-08-733-505A-56 Sequence 57, Sequence 58, Sequence 57, Sequenc	902 99.7 168 2 US-08-717-133-2 Sequence 2, A B 82.7 168 3 US-08-985-335-1 Sequence 1, A Sequence 2, A Sequence 2, A Sequence 3, A Sequence 2, A Sequence 3, A Sequence 3, A Sequence 3, A Sequence 3, A Sequence 1, A Sequence 3, A Sequence 1, A Sequence 5, A Sequence 1, A Sequence 5, A Sequence 1,	902 99.7 168 3 US-08-985-335-1 Sequence 2, A R 82.7 168 3 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US-08-455-543A-47	US-US-223-3U3C-4/ US-09-026-587-1	. US-09-227-420-1	US-08-922-865-2	US-08-986-217-6	US-08-956-242-13	US-09-351-215-13	US-09-226-012-2	US-09-226-012-4	US-08-333-565-17	US-08-661-479-17	US-09-026-587-4	US-09-227-420-4	US-08-333-565-26	US-08-661-479-26	US-09-082-737-2	US-08-906-865-4
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### ALIGNMENTS

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               61 HGGAGAVEIRSRHSSYPAGTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRWADE 120
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                                                                     Length 168;
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                                                                                                                                                                                                                                   APPLICANT: Stah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERAING SYSTEM: DOS
SOFTWARR: FastSED for Windows Version 2.0
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
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Pred. No. 2.1e-84;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                     Sequence 1, Application US/08985335
Patent No. 6080847
                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry APPLICANT: Lal, Preeti APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.78;
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Best Local Similarity 99.4
Matches 167; Conservative
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MEDIUM TYPE: Diskett
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CLONE: 358673
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STRANDEDNESS: si
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US-08-985-335-1
                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHHRQAPG-----LLMDASHOQE 53
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121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.7%; Score 748; DB 1;
83.4%; Pred. No. 9e-69;
tive 4; Mismatches
                                                                                                                                                                    STREET: Saliwanchik & Saliwanchik CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
                                                                              Sequence 2, Application US/08665617
Patent No. 5663316
                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08985335; Patent No. 6080847
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lal, Preet,
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROJERES
TITLE OF INVENTION: PROJERES
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Best Local Similarity 83.4
Matches 146; Conservative
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Lal, Preeti
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                               US-08-665-617-2
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Matches 167; Conservative
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- 2000 Compugen Ltd.
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US-08-733-505A-14
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US-08-733-505A-56
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8833 884 883 883 883 883 883 883 883 883	ULT 1 08-717-123-2 equence 2, Application U atent 00. 5965703 GENERAL INFORMATION: APPLICANT: HOTHE, Wil APPLICANT: Oltersdorf TITLE OF INVENTION: H ADDRESSE: Campbell STREET: 4370 La Jol CITY: San Diego STATE: California COUNTRY: United Sta 2.1P: 29122 COMPUTER READABLE FORM MEDIUM TYPE: Floppy COMPUTER: IBM PC CO OPERATING SYSTEM: P SOUTHOR DATE: 20-SEP CLASSIFICATION NUMBER: FILING DATE: 20-SEP CLASSIFICATION NUMBER: REFERENCE/DOCKET NUM TELECOMMUNICATION INFORMA NAMM: Campbell, Cat REFERENCE/COCKET NUM TELECHOMUNICATION INFORMA NAMM CAMPONE: (619) 535- INFORMATION FOR SEQ ID N SEQUENCE CHARACTERISTI LENGTH: 168 amino a CITYPE: anino acid TYPE: Amino acid TYPE: Amino acid	23-2 ch 1 Sir 167;
80 80 80 80 80 80 80 80 80 80 80 80 80 8	1 10-123-7 10-0 5, F 10-0	17-123 Match Local
	ULT 1 08-717-123- equence 2, atent No. 5 general INF APPLICANT TITLE OF TITLE	-08-717 Query M Best Lo Matches
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Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 QPISSSHHGGAGAVEIRSRHSSYPAGIEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRE 113
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                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL TRYORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                         2: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 748;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-2100
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ' Sequence 7, Application US/08985335
' Patent No. 6080847
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Best Local Similarity 83.4;
Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                            About
STREET: 2421 M...
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: Si
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Pred. No. 2.1e-84;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                      APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Sah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROLIFERATION
MUMBER OF SEQUENCES: 9
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bllings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                        Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
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COMPUTER: IBM Compatible
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.4:
Matches 167; Conservative
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US-08-985-335-1
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Sequence 1, Appli Sequence 1, Appli Sequence 41, Appl Sequence 1, Appli

Sequence 12,

Sequence 13 Sequence 14 Sequence 41

12, Appl 13, Appl 14, Appl 41, Appl 3, Appli 3, Appli 2, Appli 4, Appli

Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 612, Appl Sequence 612, App Sequence 1256, App Sequence 1256, App Sequence 1087, App Sequence 6082, App Sequence 6082, App Sequence 1472, App Sequence 35932, Appli Sequence 21491, Appli Sequence 235, Appli Sequence 235, Appli

Sequence 62, Appl Sequence 23468, A Sequence 113, App

Sequence 38244, A Sequence 53461, A Sequence 188802,

OM protein

Run on:

Sequence:

Searched:

Database

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REGULATING APOPTOSIS, SCREENING FOR COMPOUNDS
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                                                     PCT US98-19765-41

US-08-707-868-11

US-08-733-505-12

US-08-733-505-12

US-08-733-505-14

US-08-733-505-14

US-08-733-505-14

US-09-375-125-3

US-09-376-123-4

US-09-376-123-4

US-09-580-523-4

US-09-639-245-4

US-09-639-245-4

US-60-113-468-845-4

US-60-113-468-845-4

US-60-113-468-845-4

US-60-113-96-1087-4

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US-60-113-96-1087-4

US-60-113-96-1087-4

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US-60-113-96-1087-4

US-60-113-6082-3

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US-09-270-767-53461
US-09-270-849B-188802
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TITLE OF INVENTION: AND METHODS OF MAKING AND SCR.
TITLE OF INVENTION: AND METHODS OF MAKING AND SCR.
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: F137122
CURRENT APPLICATION NUMBER: PCT/USOU/11864
CURRENT FILING DATE: 2000-05-30
NUMBER: OF SEQ. ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-60-212-358-113
            PCT-US00-11864-2
PCT-US97-15871-1
PCT-US97-15871A-1
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PCT-USO0-11864-1
Sequence 1, Application PC/TUSO011864
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 26; Conservative
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                                                          : TYPE: PRT
ORGANISM: HOMO
PCT-US00-11864-1
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US-08-883-731-2
SEQ ID NO 1
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Sequence 2, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 32, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 21, Appli
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24.098 Million cell updates/sec
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                                                                                                      ; Search time 239.36 Seconds
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/cgn2_6/ptodata/2/paa/US098_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-375-257-2
US-09-376-154-2
US-09-410-372-1
US-09-410-372-1
US-09-587-32-1
US-09-587-473-21
PCT-US00-11864-3
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                                                                                                                                                                                                                                                                         2803329 seqs, 221847457 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US00-11864-1
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                                                                                                                                                                 US-09-580-523-1_COPY_143_168
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     October 9, 2001, 16:07:48

    protein search, using sw model

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Maximum DB seq length: 200000000
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100.0%; Score 145; DB 17;
100.0%; Pred. No. 1.6e-11;
Live 0; Mismatches 0;
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                                                                               Query Match
Best Local Similarity 100.0
Matches 26; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
; ORGANISM: Homo sapiens US-09-376-154-2
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CLONE: 358673
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US-09-410-372-1
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US-09-410-372-7
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          APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation Cell Death
FILE REFERENCE: D6120
CURRENT APPLICATION WUBBER: US/08/883,731
CURRENT FILING DATE: 1997-06-27
EARLIER APPLICATION NUMBER: US 08/665,617
EARLIER FILING DATE: 1996-06-18
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 2
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                       Length 168;
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GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Olter-Garderf, Tilman
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
TITLE REFERENCE: 480140,42802
CURRENT APPLICATION NUMBER: US/09/376,154
CURRENT FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENCODING NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Protein encoded by the BBC6 gene. US-08-883-731-2
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100.0%; Pred. No. 1.6e-11;
iive 0; Mismatches 0;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HORDE, William A.
APPLICANT: HORDE, William A.
TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCC:
TITLE OF INVENTION: ACIDS AND METHODS OF USE
FILE REFERENCE: 480140.428D1
CURRENT PILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 15
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENTH: 168
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID-NO 2
IENGTH: 168
TYPE: PRT
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Best Local Similarity 100.0
Matches 26; Conservative
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                                                                                                                                                                                                                                          ORGANISM: unknown
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US-09-376-154-2
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Sequence 1, Application US/09410372

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yew, Henry
APPLICANT: Lal, Preeti
APPLICANT: Carley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 145; DB 18; Best Local Similarity 100.0%; Pred. No. 1.6e-11; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                       E: Incyte Pharmaceuticals, Inc.
3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
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APPLICATION NUMBER: 08/985,335
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/CDOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Zhou, Xiao-Mai
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFERENCE: A7483
CURRENT APPLICATION UNDBER: US/09/580,523
CURRENT FILICATION UNDBER: 2000-05-30
NUMBER OF SEQ ID NOS: 20
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GENERAL INFORMATION:
APPLICANT: Tanay, Uyuben
TITLE OF INVENTION: Protein Knockout Technology
FILE REPERENCE: 44574-5047-W0
CURRENT FILING DATE: 2000-06-05
FRIOR APPLICATION NUMBER: US/09/587,473
CURRENT FILING DATE: 2000-06-05
FRIOR APPLICATION NUMBER: US 60/137,494
PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 145; DB 19;
Pred. No. 1.6e-11;
; Mismatches 0;
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Pred. No. 1.6e-11;
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Best Local Similarity 100.0%; Pred. No. 1.6
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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          EARLIER FILING DATE: 1994-05-27
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                                        NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-523-1
                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-357-32
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US-09-587-473-21
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SEQ ID NO 1
LENGTH: 168
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LENGTH: 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                            APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lai, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 145; DB 18; Best Local Similarity 100.0%; Pred. No. 1.6e-11; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0421 US
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APPLICATION NUMBER: 08/985,335
FILING DATE:
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APPLICANT: 3921-1-1-1
Sequence 7, Application US/09410372
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/CDCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 168 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: 1683637
US-09-410-372-7
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COUNTRY: (
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CURRENT FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 20 SOFTWARE: PatentIn Ver. 2.1
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STATE: MISSOURI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                          SEQ ID NO 2
LENGTH: 204
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                                                                                                    TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: COMPOUNDS OF MAKING AND SCREENING FOR COMPOUNDS
FILE REFERENCE: A7483
CURRENT APPLICATION UMBER: US/09/580,523
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                             Sequence 3. Application PC/TUS0011864
GENERAL INFORMATION:
APPLICANT: APOPTOSIS TECHNOLOGY, INC.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: THAT REGULATE APOPTOSIS
FILE REPERBNCE: F137122
CURRENT APPLICATION NUMBER: PCT/US00/11864
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET. 2.1
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
TITLE OF INVENTION: TAND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
TITLE, OF INVENTION: THAT REGULATE APOPTOSIS
FILE REFRENCE: F137122
CURRENT APPLICATION NUMBER: PCT/USO0/11864
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Pred. No. 3.8e-08;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 120; DB 1; 73.1%; Pred..No. 3.8e-08; tive 3; Mismatches 4,
                  137 QSAGWTRIIQSWWDRNLGKGGSTPSQ 162
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1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
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73.1%;
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Best Local Similarity 73.19
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.8
Best Local Similarity 73.1
Matches 19; Conservative
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PCT-US00-11864-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-09-580-523-3
                                                                                                RESULT 10
PCT-US00-11864-3
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MODULATION OF APOPTOSIS BY SERINE PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH REGULATOR
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                                                                               Length 204;
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Pred. No. 4.7e-08;
3; Mismatches 4; Indels
                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15871
                                                                           Score 120; DB 1;
Pred. No. 4.7e-08;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                             3: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BLVD., SUITE 1400
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PCT-US97-15871A-1
; Sequence 1, Application PC/TUS9715871A
                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      1 OSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                        ; Sequence 1, Application PC/TUS9715871
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
                                                                                                                                                                                                                                                                                                                               KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                             82.8%;
73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.8%;
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                                                                     Ouery Match
Best Local Similarity 73.1
Matches 19; Conservative
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Best Local Similarity 73.1
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                             APPLICANT: KORSMEYER, S.
TITLE OF INVENTION: MODI
TITLE OF INVENTION: PHO:
TITLE OF INVENTION: REGI
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
; ORGANISM: Mus musculus
PCT-US00-11864-2
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6029-6526

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Gaps

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82.8%; Score 120; DB 1; Length 204; 73.1%; Pred. No. 4.7e-08; Live 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
             REFERENCE/DOCKET NUMBER:
REFERENCE/DOCKET NUMBER:
FELEPONE: 314-727-5188
TELEPAX: 314-727-6092
TELEPAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
TOPOLOGY: linear
HOLESULE TYPE: protein
PCT-US98-19765-41
REGISTRATION NUMBER: 37,848
                                                                                                                                                                                                                                                                                                                                Query Match 82.89
Best Local Similarity 73.19
Matches 19; Conservative
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             APPLICANT: KORSMEYER, STANLEY J
TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
TITLE OF INVENTION: PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15871A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/19765
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GENERAL INFORMATION:
APPLICANT: WASHINGTON UNIVERSITY
TITLE OF INVENTION: CELL DEATH AGONISTS
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6029-1938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: HOLLAND DONALD R
REGISTATION UNDRER: 35,197
REFERENCE/DOCKET UNBER: 6029-
TELECOMMUNICATION INFORMATION:
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-5181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HENDERSON, MELODIE W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
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PCT-US97-15871A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
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  GENERAL INFORMATION:
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